#12

1 GACAGAGTGCAGCCTTTTCAGACTCTGTGACACAGTTCCCCTTTT
46 GCAAAAATACTTAGCGAGGATCATTACTTTCCAACAGTCGTGTCC
91 AGAGACCTACTTTGTAACACCGCAGGGAAGTTAATGTACTAGGTC
136 TTGAAAGGTCTTTCTGGAATGTGCAGTAACTTGTAGTTTTCTTCT
181 AGTAGCACTGCTAATTTTTGTGTTATAATTTTTGTAGGTCCATGG

226 GGCCGATGTATGGGAGATGAATGTGGTCCCGGAGGCATCCAAACG
MetGlyAspGluCysGlyProGlyGlyIleGlnThr

271 AGGGCTGTGTGGTGTGCTCATGTGGAGGGATGGACTACACTGCAT
ArgAlaValTrpCysAlaHisValGluGlyTrpThrThrLeuHis

316 ACTAACTGTAAGCAGGCCGAGAGACCCAATAACCAGCAGAATTGT
ThrAsnCysLysGlnAlaGluArgProAsnAsnGlnGlnAsnCys

361 TTCAAAGTTTGCGATTGGCACAAAGAGTTGTACGACTGGAGACTG
PheLysValCysAspTrpHisLysGluLeuTyrAspTrpArgLeu

406 GGACCTTGGAATCAGTGTCAGCCCGTGATTTCAAAAAGCCTAGAG
GlyProTrpAsnGlnCysGlnProValIleSerLysSerLeuGlu

451 AAACCTCTTGAGTGCATTAAGGGGGAAGAAGGTATTCAGGTGAGG
LysProLeuGluCysIleLysGlyGluGluGlyIleGlnValArg

496 GAGATAGCGTGCATCCAGAAAGACAAAGACATTCCTGCGGAGGAT
GluIleAlaCysIleGlnLysAspLysAspIleProAlaGluAsp

541 ATCATCTGTGAGTACTTTGAGCCCAAGCCTCTCCTGGAGCAGGCT
IleIleCysGluTyrPheGluProLysProLeuLeuGluGlnAla

586 TGCCTCATTCCTTGCCAGCAAGATTGCATCGTGTCTGAATTTTCT
CysLeuIleProCysGlnGlnAspCysIleValSerGluPheSer

631 GCCTGGTCCGAATGCTCCAAGACCTGCGGCAGCGGGCTCCAGCAC
AlaTrpSerGluCysSerLysThrCysGlySerGlyLeuGlnHis

676 CGGACGCGTCATGTGGTGGCGCCCCCGCAGTTCGGAGGCTCTGGC
ArgThrArgHisValValAlaProProGlnPheGlyGlySerGly

721 TGTCCAAACCTGACGGAGTTCCAGGTGTGCCAATCCAGTCCATGC
CysProAsnLeuThrGluPheGlnValCysGlnSerSerProCys

766 GAGGCCGAGGAGCTCAGGTACAGCCTGCATGTGGGGCCCTGGAGC
GluAlaGluGluLeuArgTyrSerLeuHisValGlyProTrpSer

811 ACCTGCTCAATGCCCCACTCCCGACAAGTAAGACAAGCAAGGAGA
ThrCysSerMetProHisSerArgGlnValArgGlnAlaArgArg

Fig 1

856 CGCGGGAAGAATAAAGAACGGGAAAAGGACCGCAGCAAAGGAGTA
ArgGlyLysAsnLysGluArgGluLysAspArgSerLysGlyVal

901 AAGGATCCAGAAGCCCGCGAGCTTATTAAGAAAAAGAGAAACAGA
LysAspProGluAlaArgGluLeuIleLysLysLysArgAsnArg

946 AACAGGCAGAACAGACAAGAGAACAAATATTGGGACATCCAGATT
AsnArgGlnAsnArgGlnGluAsnLysTyrTrpAspIleGlnIle

991 GGATATCAGACCAGAGAGGTTATGTGCATTAACAAGACGGGGAAA
GlyTyrGlnThrArgGluValMetCysIleAsnLysThrGlyLys

1036 GCTGCTGATTTAAGCTTTTGCCAGCAAGAGAAGCTTCCAATGACC
AlaAlaAspLeuSerPheCysGlnGlnGluLysLeuProMetThr

1081 TTCCAGTCCTGTGTGATCACCAAAGAGTGCCAGGTTTCCGAGTGG
PheGlnSerCysValIleThrLysGluCysGlnValSerGluTrp

1126 TCAGAGTGGAGCCCCTGCTCAAAAACATGCCATGACATGGTGTCC
SerGluTrpSerProCysSerLysThrCysHisAspMetValSer

1171 CCTGCAGGCACTCGTGTAAGGACACGAACCATCAGGCAGTTTCCC
ProAlaGlyThrArgValArgThrArgThrIleArgGlnPhePro

1216 ATTGGCAGTGAAAAGGAGTGTCCAGAATTTGAAGAAAAAGAACCC
IleGlySerGluLysGluCysProGluPheGluGluLysGluPro

1261 TGTTTGTCTCAAGGAGATGGAGTTGTCCCCTGTGCCACGTATGGC
CysLeuSerGlnGlyAspGlyValValProCysAlaThrTyrGly

1306 TGGAGAACTACAGAGTGGACTGAGTGCCGTGTGGACCCTTTGCTC
TrpArgThrThrGluTrpThrGluCysArgValAspProLeuLeu

1351 AGTCAGCAGGACAAGAGGCGCGGCAACCAGACGGCCCTCTGTGGA
SerGlnGlnAspLysArgArgGlyAsnGlnThrAlaLeuCysGly

1396 GGGGGCATCCAGACCCGAGAGGTGTACTGCGTGCAGGCCAACGAA
GlyGlyIleGlnThrArgGluValTyrCysValGlnAlaAsnGlu

1441 AACCTCCTCTCACAATTAAGTACCCACAAGAACAAAGAAGCCTCA
AsnLeuLeuSerGlnLeuSerThrHisLysAsnLysGluAlaSer

1486 AAGCCAATGGACTTAAAATTATGCACTGGACCTATCCCTAATACT
LysProMetAspLeuLysLeuCysThrGlyProIleProAsnThr

1531 ACACAGCTGTGCCACATTCCTTGTCCAACTGAATGTGAAGTTTCA
ThrGlnLeuCysHisIleProCysProThrGluCysGluValSer

Fig 1 (continued)

1576 CCTTGGTCAGCTTGGGGACCTTGTACTTATGAAAACTGTAATGAT
ProTrpSerAlaTrpGlyProCysThrTyrGluAsnCysAsnAsp

1621 CAGCAAGGGAAAAAAGGCTTCAAACTGAGGAAGCGGCGCATTACC
GlnGlnGlyLysLysGlyPheLysLeuArgLysArgArgIleThr

1666 AATGAGCCCACTGGAGGCTCTGGGGTAACCGGAAACTGCCCTCAC
AsnGluProThrGlyGlySerGlyValThrGlyAsnCysProHis

1711 TTACTGGAAGCCATTCCCTGTGAAGAGCCTGCCTGTTATGACTGG
LeuLeuGluAlaIleProCysGluGluProAlaCysTyrAspTrp

1756 AAAGCGGTGAGACTGGGAGACTGCGAGCCAGATAACGGAAAGGAG
LysAlaValArgLeuGlyAspCysGluProAspAsnGlyLysGlu

1801 TGTGGTCCAGGCACGCAAGTTCAAGAGGTTGTGTGCATCAACAGT
CysGlyProGlyThrGlnValGlnGluValValCysIleAsnSer

1846 GATGGAGAAGAAGTTGACAGACAGCTGTGCAGAGATGCCATCTTC
AspGlyGluGluValAspArgGlnLeuCysArgAspAlaIlePhe

1891 CCCATCCCTGTGGCCTGTGATGCCCCATGCCCGAAAGACTGTGTG
ProIleProValAlaCysAspAlaProCysProLysAspCysVal

1936 CTCAGCACATGGTCTACGTGGTCCTCCTGCTCACACACCTGCTCA
LeuSerThrTrpSerThrTrpSerSerCysSerHisThrCysSer

1981 GGGAAAACGACAGAAGGGAAACAGATACGAGCACGATCCATTCTG
GlyLysThrThrGluGlyLysGlnIleArgAlaArgSerIleLeu

2026 GCCTATGCGGGTGAAGAAGGTGGAATTCGCTGTCCAAATAGCAGT
AlaTyrAlaGlyGluGluGlyGlyIleArgCysProAsnSerSer

2071 GCTTTGCAAGAAGTACGAAGCTGTAATGAGCATCCTTGCACAGTG
AlaLeuGlnGluValArgSerCysAsnGluHisProCysThrVal

2116 TACCACTGGCAAACTGGTCCCTGGGGCCAGTGCATTGAGGACACC
TyrHisTrpGlnThrGlyProTrpGlyGlnCysIleGluAspThr

2161 TCAGTATCGTCCTTCAACACAACTACGACTTGGAATGGGGAGGCC
SerValSerSerPheAsnThrThrThrThrTrpAsnGlyGluAla

2206 TCCTGCTCTGTCGGCATGCAGACAAGAAAAGTCATCTGTGTGCGA
SerCysSerValGlyMetGlnThrArgLysValIleCysValArg

2251 GTCAATGTGGGCCAAGTGGGACCCAAAAAATGTCCTGAAAGCCTT
ValAsnValGlyGlnValGlyProLysLysCysProGluSerLeu

Fig 1 (continued)

2296 CGACCTGAAACTGTAAGGCCTTGTCTGCTTCCTTGTAAGAAGGAC
ArgProGluThrValArgProCysLeuLeuProCysLysLysAsp

2341 TGTATTGTGACCCCATATAGTGACTGGACATCATGCCCCTCTTCG
CysIleValThrProTyrSerAspTrpThrSerCysProSerSer

2386 TGTAAAGAAGGGGACTCCAGTATCAGGAAGCAGTCTAGGCATCGG
CysLysGluGlyAspSerSerIleArgLysGlnSerArgHisArg

2431 GTCATCATTCAGCTGCCAGCCAACGGGGGCCGAGACTGCACAGAT
ValIleIleGlnLeuProAlaAsnGlyGlyArgAspCysThrAsp

2476 CCCCTCTATGAAGAGAAGGCCTGTGAGGCACCTCAAGCGTGCCAA
ProLeuTyrGluGluLysAlaCysGluAlaProGlnAlaCysGln

2521 AGCTACAGGTGGAAGACTCACAAATGGCGCAGATGCCAATTAGTC
SerTyrArgTrpLysThrHisLysTrpArgArgCysGlnLeuVal

2566 CCTTGGAGCGTGCAACAAGACAGCCCTGGAGCACAGGAAGGCTGT
ProTrpSerValGlnGlnAspSerProGlyAlaGlnGluGlyCys

2611 GGGCCTGGGCGACAGGCAAGAGCCATTACTTGTCGCAAGCAAGAT
GlyProGlyArgGlnAlaArgAlaIleThrCysArgLysGlnAsp

2656 GGAGGACAGGCTGGAATCCATGAGTGCCTACAGTATGCAGGCCCT
GlyGlyGlnAlaGlyIleHisGluCysLeuGlnTyrAlaGlyPro

2701 GTGCCAGCCCTTACCCAGGCCTGCCAGATCCCCTGCCAGGATGAC
ValProAlaLeuThrGlnAlaCysGlnIleProCysGlnAspAsp

2746 TGTCAATTGACCAGCTGGTCCAAGTTTTCTTCATGCAATGGAGAC
CysGlnLeuThrSerTrpSerLysPheSerSerCysAsnGlyAsp

2791 TGTGGTGCAGTTAGGACCAGAAAGCGCACTCTTGTTGGAAAAAGT
CysGlyAlaValArgThrArgLysArgThrLeuValGlyLysSer

2836 AAAAAGAAGGAAAAATGTAAAAATTCCCATTTGTATCCCCTGATT
LysLysLysGluLysCysLysAsnSerHisLeuTyrProLeuIle

2881 GAGACTCAGTATTGTCCTTGTGACAAATATAATGCACAACCTGTG
GluThrGlnTyrCysProCysAspLysTyrAsnAlaGlnProVal

2926 GGGAACTGGTCAGACTGTATTTTACCAGAGGGAAAAGTGGAAGTG
GlyAsnTrpSerAspCysIleLeuProGluGlyLysValGluVal

2971 TTGCTGGGAATGAAAGTACAAGGAGACATCAAGGAATGCGGACAA
LeuLeuGlyMetLysValGlnGlyAspIleLysGluCysGlyGln

Fig 1 (continued)

3016 GGATATCGTTACCAAGCAATGGCATGCTACGATCAAAATGGCAGG
GlyTyrArgTyrGlnAlaMetAlaCysTyrAspGlnAsnGlyArg

3061 CTTGTGGAAACATCTAGATGTAACAGCCATGGTTACATTGAGGAG
LeuValGluThrSerArgCysAsnSerHisGlyTyrIleGluGlu

3106 GCCTGCATCATCCCCTGCCCCTCAGACTGCAAGCTCAGTGAGTGG
AlaCysIleIleProCysProSerAspCysLysLeuSerGluTrp

3151 TCCAACTGGTCGCGCTGCAGCAAGTCCTGTGGGAGTGGTGTGAAG
SerAsnTrpSerArgCysSerLysSerCysGlySerGlyValLys

3196 GTTCGTTCTAAATGGCTGCGTGAAAAACCATATAATGGAGGAAGG
ValArgSerLysTrpLeuArgGluLysProTyrAsnGlyGlyArg

3241 CCTTGCCCCAAACTGGACCATGTCAACCAGGCACAGGTGTATGAG
ProCysProLysLeuAspHisValAsnGlnAlaGlnValTyrGlu

3286 GTTGTCCCATGCCACAGTGACTGCAACCAGTACCTATGGGTCACA
ValValProCysHisSerAspCysAsnGlnTyrLeuTrpValThr

3331 GAGCCCTGGAGCATCTGCAAGGTGACCTTTGTGAATATGCGGGAG
GluProTrpSerIleCysLysValThrPheValAsnMetArgGlu

3376 AACTGTGGAGAGGGCGTGCAAACCCGAAAAGTGAGATGCATGCAG
AsnCysGlyGluGlyValGlnThrArgLysValArgCysMetGln

3421 AATACAGCAGATGGCCCTTCTGAACATGTAGAGGATTACCTCTGT
AsnThrAlaAspGlyProSerGluHisValGluAspTyrLeuCys

3466 GACCCAGAAGAGATGCCCCTGGGCTCTAGAGTGTGCAAATTACCA
AspProGluGluMetProLeuGlySerArgValCysLysLeuPro

3511 TGCCCTGAGGACTGTGTGATATCTGAATGGGGTCCATGGACCCAA
CysProGluAspCysValIleSerGluTrpGlyProTrpThrGln

3556 TGTGTTTTGCCTTGCAATCAAAGCAGTTTCCGGCAAAGGTCAGCT
CysValLeuProCysAsnGlnSerSerPheArgGlnArgSerAla

3601 GATCCCATCAGACAACCAGCTGATGAAGGAAGATCTTGCCCTAAT
AspProIleArgGlnProAlaAspGluGlyArgSerCysProAsn

3646 GCTGTTGAGAAAGAACCCTGTAACCTGAACAAAAACTGCTACCAC
AlaValGluLysGluProCysAsnLeuAsnLysAsnCysTyrHis

3691 TATGATTATAATGTAACAGACTGGAGTACATGTCAGCTGAGTGAG
TyrAspTyrAsnValThrAspTrpSerThrCysGlnLeuSerGlu

Fig 1 (continued)

3736 AAGGCAGTTTGTGGAAATGGAATAAAAACAAGGATGTTGGATTGT
LysAlaValCysGlyAsnGlyIleLysThrArgMetLeuAspCys

3781 GTTCGAAGTGATGGCAAGTCAGTTGACCTGAAATATTGTGAAGCG
ValArgSerAspGlyLysSerValAspLeuLysTyrCysGluAla

3826 CTTGGCTTGGAGAAGAACTGGCAGATGAACACGTCCTGCATGGTG
LeuGlyLeuGluLysAsnTrpGlnMetAsnThrSerCysMetVal

3871 GAATGCCCTGTGAACTGTCAGCTTTCTGATTGGTCTCCTTGGTCA
GluCysProValAsnCysGlnLeuSerAspTrpSerProTrpSer

3916 GAATGTTCTCAAACATGTGGCCTCACAGGAAAAATGATCCGAAGA
GluCysSerGlnThrCysGlyLeuThrGlyLysMetIleArgArg

3961 CGAACAGTGACCCAGCCCTTTCAAGGTGATGGAAGACCATGCCCT
ArgThrValThrGlnProPheGlnGlyAspGlyArgProCysPro

4006 TCCCTGATGGACCAGTCCAAACCCTGCCCAGTGAAGCCTTGTTAT
SerLeuMetAspGlnSerLysProCysProValLysProCysTyr

4051 CGGTGGCAATATGGCCAGTGGTCTCCATGCCAAGTGCAGGAGGCC
ArgTrpGlnTyrGlyGlnTrpSerProCysGlnValGlnGluAla

4096 CAGTGTGGAGAAGGGACCAGAACAAGGAACATTTCTTGTGTAGTA
GlnCysGlyGluGlyThrArgThrArgAsnIleSerCysValVal

4141 AGTGATGGGTCAGCTGATGATTTCAGCAAAGTGGTGGATGAGGAA
SerAspGlySerAlaAspAspPheSerLysValValAspGluGlu

4186 TTCTGTGCTGACATTGAACTCATTATAGATGGTAATAAAAATATG
PheCysAlaAspIleGluLeuIleIleAspGlyAsnLysAsnMet

4231 GTTCTGGAGGAATCCTGCAGCCAGCCTTGCCCAGGTGACTGTTAT
ValLeuGluGluSerCysSerGlnProCysProGlyAspCysTyr

4276 TTGAAGGACTGGTCTTCCTGGAGCCTGTGTCAGCTGACCTGTGTG
LeuLysAspTrpSerSerTrpSerLeuCysGlnLeuThrCysVal

4321 AATGGTGAGGATCTAGGCTTTGGTGGAATACAGGTCAGATCCAGA
AsnGlyGluAspLeuGlyPheGlyGlyIleGlnValArgSerArg

4366 CCGGTGATTATACAAGAACTAGAGAATCAGCATCTGTGCCCAGAG
ProValIleIleGlnGluLeuGluAsnGlnHisLeuCysProGlu

4411 CAGATGTTAGAAACAAAATCATGTTATGATGGACAGTGCTATGAA
GlnMetLeuGluThrLysSerCysTyrAspGlyGlnCysTyrGlu

4456 TATAAATGGATGGCCAGTGCTTGGAAGGGCTCTTCCCGAACAGTG
TyrLysTrpMetAlaSerAlaTrpLysGlySerSerArgThrVal

Fig 1 (continued)

4501 TGGTGTCAAAGGTCAGATGGTATAAATGTAACAGGGGGCTGCTTG
TrpCysGlnArgSerAspGlyIleAsnValThrGlyGlyCysLeu

4546 GTGATGAGCCAGCCTGATGCCGACAGGTCTTGTAACCCACCGTGT
ValMetSerGlnProAspAlaAspArgSerCysAsnProProCys

4591 AGTCAACCCCACTCGTACTGTAGCGAGACAAAAACATGCCATTGT
SerGlnProHisSerTyrCysSerGluThrLysThrCysHisCys

4636 GAAGAAGGGTACACTGAAGTCATGTCTTCTAACAGCACCCTTGAG
GluGluGlyTyrThrGluValMetSerSerAsnSerThrLeuGlu

4681 CAATGCACACTTATCCCCGTGGTGGTATTACCCACCATGGAGGAC
GlnCysThrLeuIleProValValValLeuProThrMetGluAsp

4726 AAAAGAGGAGATGTGAAAACCAGTCGGGCTGTACATCCAACCCAA
LysArgGlyAspValLysThrSerArgAlaValHisProThrGln

4771 CCCTCCAGTAACCCAGCAGGACGGGGAAGGACCTGGTTTCTACAG
ProSerSerAsnProAlaGlyArgGlyArgThrTrpPheLeuGln

4816 CCATTTGGGCCAGATGGGAGACTAAAGACCTGGGTTTACGGTGTA
ProPheGlyProAspGlyArgLeuLysThrTrpValTyrGlyVal

4861 GCAGCTGGGGCATTTGTGTTACTCATCTTTATTGTCTCCATGATT
AlaAlaGlyAlaPheValLeuLeuIlePheIleValSerMetIle

4906 TATCTAGCTTGCAAAAAGCCAAAGAAACCCCAAAGAAGGCAAAAC
TyrLeuAlaCysLysLysProLysLysProGlnArgArgGlnAsn

4951 AACCGACTGAAACCTTTAACCTTAGCCTATGATGGAGATGCCGAC
AsnArgLeuLysProLeuThrLeuAlaTyrAspGlyAspAlaAsp

4996 ATGTAACATATAACTTTTCCTGGCAACAACCAGTTTCGGCTTTCT
Met

Fig 1 (continued)

5041 GACTTCATAGATGTCCAGAGGCCACAACAAATGTATCCAAACTGT
5086 GTGGATTAAAATATATTTTAATTTTTAAAAATGGCATCATAAAGA
5131 CAAGAGTGAAAATCATACTGCCACTGGAGATATTTAAGACAGTAC
5176 CACTTATATACAGACCATCAACCGTGAGAATTATAGGAGATTTAG
5221 CTGAATACATGCTGCATTCTGAAAGTTTTATGTCATCTTTTCTGA
5266 AATCTACCGACTGAAAAACCACTTTCATCTCTAAAAAATAATGGT
5311 GGAATTGGCCAGTTAGGATGCCTGATACAAGACCGTCTGCAGTGT
5356 TAATCCATAAAACTTCCTAGCATGAAGAGTTTCTACCAAGATCTC
5401 CACAATACTATGGTCAAATTAACATGTGTACTCAGTTGAATGACA
5446 CACATTATGTCAGATTATGTACTTGCTAATAAGCAATTTTAACAA
5491 TGCATAACAAATAAACTCTAAGCTAAGCAGAAAATCCACTGAATA
5536 AATTCAGCATCTTGGTGGTCGATGGTAGATTTTATTGACCTGCAT
5581 TTCAGAGACAAAGCCTCTTTTTTAAGACTTCTTGTCTCTCTCCAA
5626 AGTAAGAATGCTGGACAAGTACTAGTGTCTTAGAAGAACGAGTCC
5671 TCAAGTTCAGTATTTTATAGTGGTAATTGTCTGGAAAACTAATTT
5716 ACTTGTGTTAATACAATACGTTTCTACTTTCCCTGATTTTCAAAC
5761 TGGTTGCCTGCATCTTTTTTGCTATATGGAAGGCACATTTTTGCA
5806 CTATATTAGTGCAGCACGATAGGCGCTTAACCAGTATTGCCATAG
5851 AAACTGCCTCTTTTCATGTGGGATGAAGACATCTGTGCCAAGAGT
5896 GGCATGAAGACATTTGCAAGTTCTTGTATCCTGAAGAGAGTAAAG
5941 TTCAGTTTGGATGGCAGCAAGATGAAATCAGCTATTACACCTGCT
5986 GTACACACACTTCCTCATCACTGCAGCCATTGTGAAATTGACAAC
6031 ATGGCGGTAATTTAAGTGTTGAAGTCCCTAACCCCTTAACCCTCT
6076 AAAAGGTGGATTCCTCTAGTTGGTTTGTAATTGTTCTTTGAAGGC
6121 TGTTTATGACTAGATTTTTATATTTGTTATCTTTGTTAAGAAAAA
6166 AAAAAGAAAAAGGAACTGGATGTCTTTTTAATTTTGAGCAGATGG
6211 AGAAAATAAATAATGTATCAATGACCTTTGTAACTAAAGGAAAAA
6256 AAAAAAAAATGTGGATTTTCCTTTCTCTCTGATTTCCCAGTTTCA
6301 GATTGAATGTCTGTCTTGCAGGCAGTTATTTCAAAATCCATAGTC
6346 TTTNGCCTTTCTCACTGGCAAAATTTGA

Fig 1 (continued)

```
   1  CACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCCCCTTTGGAG
  46  CCTCCTGCTGGGCCACTGGCTGGGATCAGGACACCAGTGATGGTA
  91  AGTGCTGGCCCAGACTGAAGCTCGGAGAGGCACTCTGCTTGCCCA
 136  GCGTCACAGTCTTAGCTCCCAACTGTCCTGGCTTCCAGTCTCCCT
 181  TGCTTCCCAGATCCCAGACTCTAGCCCCAGCCCCGTCTCTTTCAC
 226  CAGCTCCTGGGACCCTACGCAATCTGCGCCTGCGTCTCATCAGTC
 271  GCCCCACATGTAACTGTATCTACAACCAGCTGCACCAGCGACACC
 316  TGTCCAACCCGGCCCGGCCTGGGATGCTATGTGGGGGCCCCCAGC
 361  CTGGGGTGCAGGGCCCCTGTCAGGTCTGATAGGGAGAAGAGAAGG
 406  AGCAGAAGGGGAGGGGCCTAACCCTGGGCTGGGGGTTGGACTCAC
 451  AGGACTGGGGGAAAGAGCTGCAATCAGAGGGTGTCTGCCATAGCT
 496  GGGCTCAGGCATCTGTCCTTGGCTTTGTTGCCTGGCTCCAGGGAG
 541  ATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGACACTGGG
 586  TTCAGGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGG
 631  ACGCTCCTGTGCTGCTGACCAACACAGCTGCTCACAGTTCCTGGC
 676  TGCAGGCTCGAGTTCAGGGGGCAGCTTTCCTGGCCCAGAGCCCAG

 721  AGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGAT
                 MetSerAspGluAspSerCysValAlaCysGlyS

 766  CCTTGAGGACAGCAGGTCCCCAGGCAGGAGCACCCTCCCCATGGC
      erLeuArgThrAlaGlyProGlnAlaGlyAlaProSerProTrpP

 811  CCTGGGAGGCCAGGCTGATGCACCAGGGACAGCTGGCCTGTGGCG
      roTrpGluAlaArgLeuMetHisGlnGlyGlnLeuAlaCysGlyG

 856  GAGCCCTGGTGTCAGAGGAGGCGGTGCTAACTGCTGCCCACTGCT
      lyAlaLeuValSerGluGluAlaValLeuThrAlaAlaHisCysP

 901  TCAATGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGA
      heAsnGlyArgGlnAlaProGluGluTrpSerValGlyLeuGlyT

 946  CCAGACCGGAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAG
      hrArgProGluGluTrpGlyLeuLysGlnLeuIleLeuHisGlyA

 991  CCTACACCCACCCTGAGGGGGGCTACGACATGGCCCTCCTGCTGC
      laTyrThrHisProGluGlyGlyTyrAspMetAlaLeuLeuLeuL

1036  TGGCTCAGCCTGTGACACTGGGAGCCAGCCTGCGGGCCCTCTGCC
      euAlaGlnProValThrLeuGlyAlaSerLeuArgAlaLeuCysL

1081  TGCCCTATTTTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGG
      euProTyrPheAspHisHisLeuProAspGlyGluArgGlyTrpV

1126  TTCTGGGACGGGCCCGCCCAGGAGCAGGCATCAGCTCCCTCCAGA
      alLeuGlyArgAlaArgProGlyAlaGlyIleSerSerLeuGlnT

1171  CAGTGCCCGTGACCCTCCTGGGGCCTAGGGCCTGCAGCCGGCTGC
      hrValProValThrLeuLeuGlyProArgAlaCysSerArgLeuH
```

Fig. 2

```
1216  ATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCGGGGATGG
      isAlaAlaProGlyGlyAspGlySerProIleLeuProGlyMetV

1261  TGTGTACCAGTGCTGTGGGTGAGCTGCCCAGCTGTGAGGGCCTGT
      alCysThrSerAlaValGlyGluLeuProSerCysGluGlyLeuS

1306  CTGGGGCACCACTGGTGCATGAGGTGAGGGGCACATGGTTCCTGG
      erGlyAlaProLeuValHisGluValArgGlyThrTrpPheLeuA

1351  CCGGGCTGCACAGCTTCGGAGATGCTTGCCAAGGCCCCGCCAGGC
      laGlyLeuHisSerPheGlyAspAlaCysGlnGlyProAlaArgP

1396  CGGCGGTCTTCACCGCGCTCCCTGCCTATGAGGACTGGGTCAGCA
      roAlaValPheThrAlaLeuProAlaTyrGluAspTrpValSerS

1441  GTTTGGACTGGCAGGTCTACTTCGCCGAGGAACCAGAGCCCGAGG
      erLeuAspTrpGlnValTyrPheAlaGluGluProGluProGluA

1486  CTGAGCCTGGAAGCTGCCTGGCCAACATAAGCCAACCAACCAGCT
      laGluProGlySerCysLeuAlaAsnIleSerGlnProThrSerC

1531  GCTGACAGGGGACCTGGCCATTCTCAGGACAAGAGAATGCAGGCA
      ys

1576  GGCAAATGGCATTACTGCCCCTGTCCTCCCCACCCTGTCATGTGT
1621  GATTCCAGGCACCAGGGCAGGCCCAGAAGCCCAGCAGCTGTGGGA
1666  AGGAACCTGCCTGGGGCCACAGGTGCCCCCTCCCCACCCTGCAGG
1711  ACAGGGGTGTCTGTGGACACTCCCACACCCAACTCTGCTACCAAG
1756  CAGGCGTCTCAGCTTTCCTCCTCCTTTACCCTTTCAGATACAATC
1801  ACGCCAGCCCCGTTGTTTTGAAAATTTCTTTTTTTGGGGGGCAGC
1846  AGTTTTCCTTTTTTTAAACTTAAATAAATTGTTACAAAATAGACT
1891  TTAG
```

Fig. 2 (continued)

```
  1 GCGGATCCTCACACGACTGTGATCCGATTCTTTCCAGCGGCTTCT
 46 GCAACCAAGCGGGTCTTACCCCCGGTCCTCCGCGTCTCCAGTCCT
 91 CGCACCTGGAACCCCAACGTCCCCGAGAGTCCCCGAATCCCCGCT

136 CCCAGGCTACCTAAGAGGATGAGCGGTGCTCCGACGGCCGGGGCA
                                MetSerGlyAlaProThrAlaGlyAla

181 GCCCTGATGCTCTGCGCCGCCACCGCCGTGCTACTGAGCGCTCAG
    AlaLeuMetLeuCysAlaAlaThrAlaValLeuLeuSerAlaGln

226 GGCGGACCCGTGCAGTCCAAGTCGCCGCGCTTTGCGTCCTGGGAC
    GlyGlyProValGlnSerLysSerProArgPheAlaSerTrpAsp

271 GAGATGAATGTCCTGGCGCACGGACTCCTGCAGCTCGGCCAGGGG
    GluMetAsnValLeuAlaHisGlyLeuLeuGlnLeuGlyGlnGly

316 TGCGCGAACACCGGAGCGCACCCGCAGTCAGCTGAGCGCGCTGGA
    CysAlaAsnThrGlyAlaHisProGlnSerAlaGluArgAlaGly

361 GCGCGCCTGAGCGCGTGCGGGTCCGCCTGTCAGGGAACCGAGGGG
    AlaArgLeuSerAlaCysGlySerAlaCysGlnGlyThrGluGly

406 TCCACCGACCTCCCGTTAGCCCCTGAGAGCCGGGTGGACCCTGAG
    SerThrAspLeuProLeuAlaProGluSerArgValAspProGlu

451 GTCCTTCACAGCCTGCAGACACAACTCAAGGCTCAGAACAGCAGG
    ValLeuHisSerLeuGlnThrGlnLeuLysAlaGlnAsnSerArg

496 ATCCAGCAACTCTTCCACAAGGTGGCCCAGCAGCAGCGGCACCTG
    IleGlnGlnLeuPheHisLysValAlaGlnGlnGlnArgHisLeu

541 GAGAAGCAGCACCTGCGAATTCAGCATCTGCAAAGCCAGTTTGGC
    GluLysGlnHisLeuArgIleGlnHisLeuGlnSerGlnPheGly

586 CTCCTGGACCACAAGCACCTAGACCATGAGGTGGCCAAGCCTGCC
    LeuLeuAspHisLysHisLeuAspHisGluValAlaLysProAla

631 CGAAGAAAGAGGCTGCCCGAGATGGCCCAGCCAGTTGACCCGGCT
    ArgArgLysArgLeuProGluMetAlaGlnProValAspProAla

676 CACAATGTCAGCCGCCTGCACCGGCTGCCCAGGGATTGCCAGGAG
    HisAsnValSerArgLeuHisArgLeuProArgAspCysGlnGlu

721 CTGTTCCAGGTTGGGGAGAGGCAGAGTGGACTATTTGAAATCCAG
    LeuPheGlnValGlyGluArgGlnSerGlyLeuPheGluIleGln

766 CCTCAGGGGTCTCCGCCATTTTTGGTGAACTGCAAGATGACCTCA
    ProGlnGlySerProProPheLeuValAsnCysLysMetThrSer
```

Fig. 3

811 GATGGAGGCTGGACAGTAATTCAGAGGCGCCACGATGGCTCAGTG
AspGlyGlyTrpThrValIleGlnArgArgHisAspGlySerVal

856 GACTTCAACCGGCCCTGGGAAGCCTACAAGGCGGGGTTTGGGGAT
AspPheAsnArgProTrpGluAlaTyrLysAlaGlyPheGlyAsp

901 CCCCACGGCGAGTTCTGGCTGGGTCTGGAGAAGGTGCATAGCATG
ProHisGlyGluPheTrpLeuGlyLeuGluLysValHisSerMet

946 ATGGGGGACCGCAACAGCCGCCTGGCCGTGCAGCTGCGGGACTGG
MetGlyAspArgAsnSerArgLeuAlaValGlnLeuArgAspTrp

991 GATGGCAACGCCGAGTTGCTGCAGTTCTCCGTGCACCTGGGTGGC
AspGlyAsnAlaGluLeuLeuGlnPheSerValHisLeuGlyGly

1036 GAGGACACGGCCTATAGCCTGCAGCTCACTGCACCCGTGGCCGGC
GluAspThrAlaTyrSerLeuGlnLeuThrAlaProValAlaGly

1081 CAGCTGGGCGCCACCACCGTCCCACCCAGCGGCCTCTCCGTACCC
GlnLeuGlyAlaThrThrValProProSerGlyLeuSerValPro

1126 TTCTCCACTTGGGACCAGGATCACGACCTCCGCAGGGACAAGAAC
PheSerThrTrpAspGlnAspHisAspLeuArgArgAspLysAsn

1171 TGCGCCAAGAGCCTCTCTGGAGGCTGGTGGTTTGGCACCTGCAGC
CysAlaLysSerLeuSerGlyGlyTrpTrpPheGlyThrCysSer

1216 CATTCCAACCTCAACGGCCAGTACTTCCGCTCCATCCCACAGCAG
HisSerAsnLeuAsnGlyGlnTyrPheArgSerIleProGlnGln

1261 CGGCAGAAGCTTAAGAAGGGAATCTTCTGGAAGACCTGGCGGGGC
ArgGlnLysLeuLysLysGlyIlePheTrpLysThrTrpArgGly

1306 CGCTACTACCCGCTGCAGGCCACCACCATGTTGATCCAGCCCATG
ArgTyrTyrProLeuGlnAlaThrThrMetLeuIleGlnProMet

1351 GCAGCAGAGGCAGCCTCCTAGCGTCCTGGCTGGGCCTGGTCCCAG
AlaAlaGluAlaAlaSer

1396 GCCCACGAAAGACGGTGACTCTTGGCTCTGCCCGAGGATGTGGCC
1441 GTTCCCTGCCTGGGCAGGGGCTCCAAGGAGGGGCCATCTGGAAAC
1486 TTGTGGACAGAGAAGAAGACCACGACTGGAGAAGCCCCCTTTCTG
1531 AGTGCAGGGGGGCTGCATGCGTTGCCTCCTGAGATCGAGGCTGCA
1576 GGATATGCTCAGACTCTAGAGGCGTGGACCAAGGGGCATGGAGCT
1621 TCACTCCTTGCTGGCCAGGGAGTTGGGGACTCAGAGGGACCACTT
1666 GGGGCCAGCCAGACTGGCCTCAATGGCGGACTCAGTCACATTGAC
1711 TGACGGGGACCAGGGCTTGTGTGGGTCGAGAGCGCCCTCATGGTG
1756 CTGGTGCTGTTGTGTGTAGGTCCCCTGGGGACACAAGCAGGCGCC
1801 AATGGTATCTGGGCGGAGCTCACAGAGTTCTTGGAATAAAAGCAA
1846 CCTCAGAACA

Fig. 3 (continued)

1 GGTAGCCGACGCGCCGGCCGGCGCGTGACCTTGCCCCTCTTGCTC

46 GCCTTGAAAATGGAAAAGATGCTCGCAGGCTGCTTTCTGCTGATC
MetGluLysMetLeuAlaGlyCysPheLeuLeuIle

91 CTCGGACAGATCGTCCTCCTCCCTGCCGAGGCCAGGGAGCGGTCA
LeuGlyGlnIleValLeuLeuProAlaGluAlaArgGluArgSer

136 CGTGGGAGGTCCATCTCTAGGGGCAGACACGCTCGGACCCACCCG
ArgGlyArgSerIleSerArgGlyArgHisAlaArgThrHisPro

181 CAGACGGCCCTTCTGGAGAGTTCCTGTGAGAACAAGCGGGCAGAC
GlnThrAlaLeuLeuGluSerSerCysGluAsnLysArgAlaAsp

226 CTGGTTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGAC
LeuValPheIleIleAspSerSerArgSerValAsnThrHisAsp

271 TATGCAAAGGTCAAGGAGTTCATCGTGGACATCTTGCAATTCTTG
TyrAlaLysValLysGluPheIleValAspIleLeuGlnPheLeu

316 GACATTGGTCCTGATGTCACCCGAGTGGGCCTGCTCCAATATGGC
AspIleGlyProAspValThrArgValGlyLeuLeuGlnTyrGly

361 AGCACTGTCAAGAATGAGTTCTCCCTCAAGACCTTCAAGAGGAAG
SerThrValLysAsnGluPheSerLeuLysThrPheLysArgLys

406 TCCGAGGTGGAGCGTGCTGTCAAGAGGATGCGGCATCTGTCCACG
SerGluValGluArgAlaValLysArgMetArgHisLeuSerThr

451 GGCACCATGACTGGGCTGGCCATCCAGTATGCCCTGAACATCGCA
GlyThrMetThrGlyLeuAlaIleGlnTyrAlaLeuAsnIleAla

496 TTCTCAGAAGCAGAGGGGGCCCGGCCCCTGAGGGAGAATGTGCCA
PheSerGluAlaGluGlyAlaArgProLeuArgGluAsnValPro

541 CGGGTCATAATGATCGTGACGGATGGGAGACCTCAGGACTCCGTG
ArgValIleMetIleValThrAspGlyArgProGlnAspSerVal

586 GCCGAGGTGGCTGCTAAGGCACGGGACACGGGCATCCTAATCTTT
AlaGluValAlaAlaLysAlaArgAspThrGlyIleLeuIlePhe

631 GCCATTGGTGTGGGCCAGGTAGACTTCAACACCTTGAAGTCCATT
AlaIleGlyValGlyGlnValAspPheAsnThrLeuLysSerIle

676 GGGAGTGAGCCCCATGAGGACCATGTCTTCCTTGTGGCCAATTTC
GlySerGluProHisGluAspHisValPheLeuValAlaAsnPhe

721 AGCCAGATTGAGACGCTGACCTCCGTGTTCCAGAAGAAGTTGTGC
SerGlnIleGluThrLeuThrSerValPheGlnLysLysLeuCys

Fig. 4

766 ACGGCCCACATGTGCAGCACCCTGGAGCATAACTGTGCCCACTTC
ThrAlaHisMetCysSerThrLeuGluHisAsnCysAlaHisPhe

811 TGCATCAACATCCCTGGCTCATACGTCTGCAGGTGCAAACAAGGC
CysIleAsnIleProGlySerTyrValCysArgCysLysGlnGly

856 TACATTCTCAACTCGGATCAGACGACTTGCAGAATCCAGGATCTG
TyrIleLeuAsnSerAspGlnThrThrCysArgIleGlnAspLeu

901 TGTGCCATGGAGGACCACAACTGTGAGCAGCTCTGTGTGAATGTG
CysAlaMetGluAspHisAsnCysGluGlnLeuCysValAsnVal

946 CCGGGCTCCTTCGTCTGCGAGTGCTACAGTGGCTACGCCCTGGCT
ProGlySerPheValCysGluCysTyrSerGlyTyrAlaLeuAla

991 GAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCCTCAGAA
GluAspGlyLysArgCysValAlaValAspTyrCysAlaSerGlu

1036 AACCACGGATGTGAACATGAGTGTGTAAATGCTGATGGCTCCTAC
AsnHisGlyCysGluHisGluCysValAsnAlaAspGlySerTyr

1081 CTTTGCCAGTGCCATGAAGGATTTGCTCTTAACCCAGATGAAAAA
LeuCysGlnCysHisGluGlyPheAlaLeuAsnProAspGluLys

1126 ACGTGCACAAAGATAGACTACTGTGCCTCATCTAATCATGGATGT
ThrCysThrLysIleAspTyrCysAlaSerSerAsnHisGlyCys

1171 CAGTACGAGTGTGTTAACACAGATGATTCCTATTCCTGCCACTGC
GlnTyrGluCysValAsnThrAspAspSerTyrSerCysHisCys

1216 CTGAAAGGCTTTACCCTGAATCCAGATAAGAAAACCTGCAGAAGG
LeuLysGlyPheThrLeuAsnProAspLysLysThrCysArgArg

1261 ATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGC
IleAsnTyrCysAlaLeuAsnLysProGlyCysGluHisGluCys

1306 GTCAACATGGAGGAGAGCTACTACTGCCGCTGCCACCGTGGCTAC
ValAsnMetGluGluSerTyrTyrCysArgCysHisArgGlyTyr

1351 ACTCTGGACCCCAATGGCAAACCCTGCAGCCGAGTGGACCACTGT
ThrLeuAspProAsnGlyLysProCysSerArgValAspHisCys

1396 GCACAGCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGGAG
AlaGlnGlnAspHisGlyCysGluGlnLeuCysLeuAsnThrGlu

1441 GATTCCTTCGTCTGCCAGTGCTCAGAAGGCTTCCTCATCAACGAG
AspSerPheValCysGlnCysSerGluGlyPheLeuIleAsnGlu

Fig. 4 (continued)

1486 GACCTCAAGACCTGCTCCCGGGTGGATTACTGCCTGCTGAGTGAC
AspLeuLysThrCysSerArgValAspTyrCysLeuLeuSerAsp

1531 CATGGTTGTGAATACTCCTGTGTCAACATGGACAGATCCTTTGCC
HisGlyCysGluTyrSerCysValAsnMetAspArgSerPheAla

1576 TGTCAGTGTCCTGAGGGACACGTGCTCCGCAGCGATGGAAGACG
CysGlnCysProGluGlyHisValLeuArgSerAspGlyLysThr

1621 TGTGCAAAATTGGACTCTTGTGCTCTGGGGGACCACGGTTGTGAA
CysAlaLysLeuAspSerCysAlaLeuGlyAspHisGlyCysGlu

1666 CATTCGTGTGTAAGCAGTGAAGATTCGTTTGTGTGCCAGTGCTTT
HisSerCysValSerSerGluAspSerPheValCysGlnCysPhe

1711 GAAGGTTATATACTCCGTGAAGATGGAAAAACCTGCAGAAGGAAA
GluGlyTyrIleLeuArgGluAspGlyLysThrCysArgArgLys

1756 GATGTCTGCCAAGCTATAGACCATGGCTGTGAACACATTTGTGTG
AspValCysGlnAlaIleAspHisGlyCysGluHisIleCysVal

1801 AACAGTGACGACTCATACACGTGCGAGTGCTTGGAGGGATTCCGG
AsnSerAspAspSerTyrThrCysGluCysLeuGluGlyPheArg

1846 CTCACTGAGGATGGGAAACGCTGCCGAATTTCCTCAGGGAAGGAT
LeuThrGluAspGlyLysArgCysArgIleSerSerGlyLysAsp

1891 GTCTGCAAATCAACCCACCATGGCTGCGAACACATTTGTGTTAAT
ValCysLysSerThrHisHisGlyCysGluHisIleCysValAsn

1936 AATGGGAATTCCTACATCTGCAAATGCTCAGAGGGATTTGTTCTA
AsnGlyAsnSerTyrIleCysLysCysSerGluGlyPheValLeu

1981 GCTGAGGACGGAAGACGGTGCAAGAAATGCACTGAAGGCCCAATT
AlaGluAspGlyArgArgCysLysLysCysThrGluGlyProIle

2026 GACCTGGTCTTTGTGATCGATGGATCCAAGAGTCTTGGAGAAGAG
AspLeuValPheValIleAspGlySerLysSerLeuGlyGluGlu

2071 AATTTTGAGGTCGTGAAGCAGTTTGTCACTGGAATTATAGATTCC
AsnPheGluValValLysGlnPheValThrGlyIleIleAspSer

2116 TTGACAATTTCCCCCAAAGCCGCTCGAGTGGGGCTGCTCCAGTAT
LeuThrIleSerProLysAlaAlaArgValGlyLeuLeuGlnTyr

2161 TCCACACAGGTCCACACAGAGTTCACTCTGAGAAACTTCAACTCA
SerThrGlnValHisThrGluPheThrLeuArgAsnPheAsnSer

2206 GCCAAAGACATGAAAAAAGCCGTGGCCCACATGAAATACATGGGA
AlaLysAspMetLysLysAlaValAlaHisMetLysTyrMetGly

Fig. 4 (continued)

```
2251   AAGGGCTCTATGACTGGGCTGGCCCTGAAACACATGTTTGAGAGA
       LysGlySerMetThrGlyLeuAlaLeuLysHisMetPheGluArg

2296   AGTTTTACCCAAGGAGAAGGGGCCAGGCCCCTTTTCCACAAGGGT
       SerPheThrGlnGlyGluGlyAlaArgProLeuPheHisLysGly

2341   GCCCAGAGCAGCCATTGTGTTCACCGACGGACGGGCTCAGGATGA
       AlaGlnSerSerHisCysValHisArgArgThrGlySerGly

2386   CGTCTCCGAGTGGGCCAGTAAAGCCAAGGCCAATGGTATCACTAT
2431   GTATGCTGTTGGGGTAGGAAAAGCCATTGAGGAGGAACTACAAGA
2476   GATTGCCTCTGAGCCCACAAACAAGCATCTCTTCTATGCCGAAGA
2521   CTTCAGCACAATGGATGAGATAAGTGAAAAACTCAAGAAAGGCAT
2566   CTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAGC
2611   AGGGGAACTGCCAAAAACGGTCCAACAGCCAACAGAATCTGAGCC
2656   AGTCACCATAAATATCCAAGACCTACTTTCCTGTTCTAATTTTGC
2701   AGTGCAACACAGATATCTGTTTGAAGAAGACAATCTTTTACGGTC
2746   TACACAAAAGCTTTCCCATTCAACAAAACCTTCAGGAAGCCCTTT
2791   GGAAGAAAAACACGATCAATGCAAATGTGAAAACCTTATAATGTT
2836   CCAGAACCTTGCAAACGAAGAAGTAAGAAAATTTACACAGCGCTT
2881   AGAAGAAATGACACAGAGAATGGAAGCCCTGGAAAATCGCCTGAG
2926   ATACAGATGAAGATTAGAAATCGCGACACATTTGTAGTCATTGTA
2971   TCACGGATTACAATGAACGCAGTGCAGAGCCCCAAAGCTCAGGCT
3016   ATTGTTAAATC
```

Fig. 4 (continued)

1 GGTAGCCGACGCGCCGGCCGGCGCGTGACCTTGCCCCTCTTGCTC

46 GCCTTGAAAATGGAAAAGATGCTCGCAGGCTGCTTTCTGCTGATC
MetGluLysMetLeuAlaGlyCysPheLeuLeuIle

91 CTCGGACAGATCGTCCTCCTCCCCTGCGAGGCCAGGGAGCGGTCA
LeuGlyGlnIleValLeuLeuProCysGluAlaArgGluArgSer

136 CGTGGGAGGTCCATCTCTAGGGGCAGACACGCTCGGACCCACCCG
ArgGlyArgSerIleSerArgGlyArgHisAlaArgThrHisPro

181 CAGACGGCCCTTCTGGAGAGTTCCTGTGAGAACAAGCGGGCAGAC
GlnThrAlaLeuLeuGluSerSerCysGluAsnLysArgAlaAsp

226 CTGGTTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGAC
LeuValPheIleIleAspSerSerArgSerValAsnThrHisAsp

271 TATGCAAAGGTCAAGGAGTTCATCGTGGACATCTTGCAATTCTTG
TyrAlaLysValLysGluPheIleValAspIleLeuGlnPheLeu

316 GACATTGGTCCTGATGTCACCCGAGTGGGCCTGCTCCAATATGGC
AspIleGlyProAspValThrArgValGlyLeuLeuGlnTyrGly

361 AGCACTGTCAAGAATGAGTTCTCCCTCAAGACCTTCAAGAGGAAG
SerThrValLysAsnGluPheSerLeuLysThrPheLysArgLys

406 TCCGAGGTGGAGCGTGCTGTCAAGAGGATGCGGCATCTGTCCACG
SerGluValGluArgAlaValLysArgMetArgHisLeuSerThr

451 GGCACCATGACTGGGCTGGCCATCCAGTATGCCCTGAACATCGCA
GlyThrMetThrGlyLeuAlaIleGlnTyrAlaLeuAsnIleAla

496 TTCTCAGAAGCAGAGGGGGCCCGGCCCCTGAGGGAGAATGTGCCA
PheSerGluAlaGluGlyAlaArgProLeuArgGluAsnValPro

541 CGGGTCATAATGATCGTGACGGATGGGAGACCTCAGGACTCCGTG
ArgValIleMetIleValThrAspGlyArgProGlnAspSerVal

586 GCCGAGGTGGCTGCTAAGGCACGGGACACGGGCATCCTAATCTTT
AlaGluValAlaAlaLysAlaArgAspThrGlyIleLeuIlePhe

631 GCCATTGGTGTGGGCCAGGTAGACTTCAACACCTTGAAGTCCATT
AlaIleGlyValGlyGlnValAspPheAsnThrLeuLysSerIle

676 GGGAGTGAGCCCCATGAGGACCATGTCTTCCTTGTGGCCAATTTC
GlySerGluProHisGluAspHisValPheLeuValAlaAsnPhe

721 AGCCAGATTGAGACGCTGACCTCCGTGTTCCAGAAGAAGTTGTGC
SerGlnIleGluThrLeuThrSerValPheGlnLysLysLeuCys

Fig. 5

766 ACGGCCCACATGTGCAGCACCCTGGAGCATAACTGTGCCCACTTC
ThrAlaHisMetCysSerThrLeuGluHisAsnCysAlaHisPhe

811 TGCATCAACATCCCTGGCTCATACGTCTGCAGGTGCAAACAAGGC
CysIleAsnIleProGlySerTyrValCysArgCysLysGlnGly

856 TACATTCTCAACTCGGATCAGACGACTTGCAGAATCCAGGATCTG
TyrIleLeuAsnSerAspGlnThrThrCysArgIleGlnAspLeu

901 TGTGCCATGGAGGACCACAACTGTGAGCAGCTCTGTGTGAATGTG
CysAlaMetGluAspHisAsnCysGluGlnLeuCysValAsnVal

946 CCGGGCTCCTTCGTCTGCGAGTGCTACAGTGGCTACGCCCTGGCT
ProGlySerPheValCysGluCysTyrSerGlyTyrAlaLeuAla

991 GAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCCTCAGAA
GluAspGlyLysArgCysValAlaValAspTyrCysAlaSerGlu

1036 AACCACGGATGTGAACATGAGTGTGTAAATGCTGATGGCTCCTAC
AsnHisGlyCysGluHisGluCysValAsnAlaAspGlySerTyr

1081 CTTTGCCAGTGCCATGAAGGATTTGCTCTTAACCCAGATGAAAAA
LeuCysGlnCysHisGluGlyPheAlaLeuAsnProAspGluLys

1126 ACGTGCACAAAGATAGACTACTGTGCCTCATCTAATCATGGATGT
ThrCysThrLysIleAspTyrCysAlaSerSerAsnHisGlyCys

1171 CAGTACGAGTGTGTTAACACAGATGATTCCTATTCCTGCCACTGC
GlnTyrGluCysValAsnThrAspAspSerTyrSerCysHisCys

1216 CTGAAAGGCTTTACCCTGAATCCAGATAAGAAAACCTGCAGAAGG
LeuLysGlyPheThrLeuAsnProAspLysLysThrCysArgArg

1261 ATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGC
IleAsnTyrCysAlaLeuAsnLysProGlyCysGluHisGluCys

1306 GTCAACATGGAGGAGAGCTACTACTGCCGCTGCCACCGTGGCTAC
ValAsnMetGluGluSerTyrTyrCysArgCysHisArgGlyTyr

1351 ACTCTGGACCCCAATGGCAAAACCCTGCAGCCGAGTGGACCACTGT
ThrLeuAspProAsnGlyLysProCysSerArgValAspHisCys

1396 GCACAGCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGGAG
AlaGlnGlnAspHisGlyCysGluGlnLeuCysLeuAsnThrGlu

1441 GATTCCTTCGTCTGCCAGTGCTCAGAAGGCTTCCTCATCAACGAG
AspSerPheValCysGlnCysSerGluGlyPheLeuIleAsnGlu

1486 GACCTCAAGACCTGCTCCCGGGTGGATTACTGCCTGCTGAGTGAC
AspLeuLysThrCysSerArgValAspTyrCysLeuLeuSerAsp

Fig. 5 (continued)

1531 CATGGTTGTGAATACTCCTGTGTCAACATGGACAGATCCTTTGCC
HisGlyCysGluTyrSerCysValAsnMetAspArgSerPheAla

1576 TGTCAGTGTCCTGAGGGACACGTGCTCCGCAGCGATGGGAAGACG
CysGlnCysProGluGlyHisValLeuArgSerAspGlyLysThr

1621 TGTGCAAAATTGGACTCTTGTGCTCTGGGGGACCACGGTTGTGAA
CysAlaLysLeuAspSerCysAlaLeuGlyAspHisGlyCysGlu

1666 CATTCGTGTGTAAGCAGTGAAGATTCGTTTGTGTGCCAGTGCTTT
HisSerCysValSerSerGluAspSerPheValCysGlnCysPhe

1711 GAAGGTTATATACTCCGTGAAGATGGAAAAACCTGCAGAAGGAAA
GluGlyTyrIleLeuArgGluAspGlyLysThrCysArgArgLys

1756 GATGTCTGCCAAGCTATAGACCATGGCTGTGAACACATTTGTGTG
AspValCysGlnAlaIleAspHisGlyCysGluHisIleCysVal

1801 AACAGTGACGACTCATACACGTGCGAGTGCTTGGAGGGATTCCGG
AsnSerAspAspSerTyrThrCysGluCysLeuGluGlyPheArg

1846 CTCACTGAGGATGGGAAACGCTGCCGAATTTCCTCAGGGAAGGAT
LeuThrGluAspGlyLysArgCysArgIleSerSerGlyLysAsp

1891 GTCTGCAAATCAACCCACCATGGCTGCGAACACATTTGTGTTAAT
ValCysLysSerThrHisHisGlyCysGluHisIleCysValAsn

1936 AATGGGAATTCCTACATCTGCAAATGCTCAGAGGGATTTGTTCTA
AsnGlyAsnSerTyrIleCysLysCysSerGluGlyPheValLeu

1981 GCTGAGGACGGAAGACGGTGCAAGAAATGCACTGAAGGCCCAATT
AlaGluAspGlyArgArgCysLysLysCysThrGluGlyProIle

2026 GACCTGGTCTTTGTGATCGATGGATCCAAGAGTCTTGGAGAAGAG
AspLeuValPheValIleAspGlySerLysSerLeuGlyGluGlu

2071 AATTTTGAGGTCGTGAAGCAGTTTGTCACTGGAATTATAGATTCC
AsnPheGluValValLysGlnPheValThrGlyIleIleAspSer

2116 TTGACAATTTCCCCCAAAGCCGCTCGAGTGGGGCTGCTCCAGTAT
LeuThrIleSerProLysAlaAlaArgValGlyLeuLeuGlnTyr

2161 TCCACACAGGTCCACACAGAGTTCACTCTGAGAAACTTCAACTCA
SerThrGlnValHisThrGluPheThrLeuArgAsnPheAsnSer

2206 GCCAAAGACATGAAAAAAGCCGTGGCCCACATGAAATACATGGGA
AlaLysAspMetLysLysAlaValAlaHisMetLysTyrMetGly

Fig. 5 (continued)

2251 AAGGGCTCTATGACTGGGCTGGCCCTGAAACACATGTTTGAGAGA
LysGlySerMetThrGlyLeuAlaLeuLysHisMetPheGluArg

2296 AGTTTTACCCAAGGAGAAGGGGCCAGGCCCTTTTCCACAAGGGTG
SerPheThrGlnGlyGluGlyAlaArgProPheSerThrArgVal

2341 CCCAGAGCAGCCATTGTGTTCACCGACGGACGGGCTCAGGATGAC
ProArgAlaAlaIleValPheThrAspGlyArgAlaGlnAspAsp

2386 GTCTCCGAGTGGGCCAGTAAAGCCAAGGCCAATGGTATCACTATG
ValSerGluTrpAlaSerLysAlaLysAlaAsnGlyIleThrMet

2431 TATGCTGTTGGGGTAGGAAAAGCCATTGAGGAGGAACTACAAGAG
TyrAlaValGlyValGlyLysAlaIleGluGluGluLeuGlnGlu

2476 ATTGCCTCTGAGCCCACAAACAAGCATCTCTTCTATGCCGAAGAC
IleAlaSerGluProThrAsnLysHisLeuPheTyrAlaGluAsp

2521 TTCAGCACAATGGATGAGATAAGTGAAAAACTCAAGAAAGGCATC
PheSerThrMetAspGluIleSerGluLysLeuLysLysGlyIle

2566 TGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAGCA
CysGluAlaLeuGluAspSerAspGlyArgGlnAspSerProAla

2611 GGGGAACTGCCAAAAACGGTCCAACAGCCAACAGAATCTGAGCCA
GlyGluLeuProLysThrValGlnGlnProThrGluSerGluPro

2656 GTCACCATAAATATCCAAGACCTACTTTCCTGTTCTAATTTTGCA
ValThrIleAsnIleGlnAspLeuLeuSerCysSerAsnPheAla

2701 GTGCAACACAGATATCTGTTTGAAGAAGACAATCTTTTACGGTCT
ValGlnHisArgTyrLeuPheGluGluAspAsnLeuLeuArgSer

2746 ACACAAAAGCTTTCCCATTCAACAAAACCTTCAGGAAGCCCTTTG
ThrGlnLysLeuSerHisSerThrLysProSerGlySerProLeu

2791 GAAGAAAAACACGATCAATGCAAATGTGAAAACCTTATAATGTTC
GluGluLysHisAspGlnCysLysCysGluAsnLeuIleMetPhe

2836 CAGAACCTTGCAAACGAAGAAGTAAGAAAATTAACACAGCGCTTA
GlnAsnLeuAlaAsnGluGluValArgLysLeuThrGlnArgLeu

2881 GAAGAAATGACACAGAGAATGGAAGCCCTGGAAAATCGCCTGAGA
GluGluMetThrGlnArgMetGluAlaLeuGluAsnArgLeuArg

2926 TACAGATGAAGATTAGAAATCGCGACACATTTGTAGTCATTGTAT
TyrArg

Fig. 5 (continued)

2971 CACGGATTACAATGAACGCAGTGCAGAGCCCCAAAGCTCAGGCTA
3016 TTGTTAAATCAATAATGTTGTGAAGTAAAACAATCAGTACTGAGA
3061 AACCTGGTTTGCCACAGAACAAAGACAAGAAGTATACACTAACTT
3106 GTATAAATTTATCTAGGAAAAAAATCCTTCAGAATTCTAAGATGA
3151 ATTTACCAGGTGAGAATGAATAAGCTATGCAAGGTATTTTGTAAT
3196 ATACTGTGGACACAACTTGCTTCTGCCTCATCCTGCCTTAGTGTG
3241 CAATCTCATTTGACTATACGATAAAGTTTGCACAGTCTTACTTCT
3286 GTAGAACACTGGCCATAGGAAATGCTGTTTTTTTGTACTGGACTT
3331 TACCTTGATATATGTATATGGATGTATGCATAAAATCATAGGACA
3376 TATGTACTTGTGGAACAAGTTGGATTTTTTATACAATATTAAAAT
3421 TCACCACTTCAGAGAAAAGTAAAAAAA

Fig. 5 (continued)

```
  1 CGGCCCTTCTCACACTCCTGCCCTGCTGATGTGGAACGGGGTTTG
 46 GGGTTCTGCAGGGCTATTGTCTGCGCTGGGGAAGGGGACAGGCCG
 91 GGACCGGGACCTCCGCTCGCAGCCGGCCGCACCAGCAGGACAGCT

136 GGCCTGAAGCTCAGAGCCGGGGCGTGCGCCATGGCCCCACACTGG
                                  MetAlaProHisTrp

181 GCTGTCTGGCTGCTGGCAGCAAGGCTGTGGGGCCTGGGCATTGGG
    AlaValTrpLeuLeuAlaAlaArgLeuTrpGlyLeuGlyIleGly

226 GCTGAGGTGTGGTGGAACCTTGTGCCGCGTAAGACAGTGTCTTCT
    AlaGluValTrpTrpAsnLeuValProArgLysThrValSerSer

271 GGGGAGCTGGCCACGGTAGTACGGCGGTTCTCCCAGACCGGCATC
    GlyGluLeuAlaThrValValArgArgPheSerGlnThrGlyIle

316 CAGGACTTCCTGACACTGACGCTGACGGAGCCCACTGGGCTTCTG
    GlnAspPheLeuThrLeuThrLeuThrGluProThrGlyLeuLeu

361 TACGTGGGCGCCCGAGAGGCCCTGTTTGCCTTCAGCATGGAGGCC
    TyrValGlyAlaArgGluAlaLeuPheAlaPheSerMetGluAla

406 CTGGAGCTGCAAGGAGCGATCTCCTGGGAGGCCCCCGTGGAGAAG
    LeuGluLeuGlnGlyAlaIleSerTrpGluAlaProValGluLys

451 AAGACTGAGTGTATCCAGAAAGGGAAGAACAACCAGACCGAGTGC
    LysThrGluCysIleGlnLysGlyLysAsnAsnGlnThrGluCys

496 TTCAACTTCATCCGCTTCCTGCAGCCCTACAATGCCTCCCACCTG
    PheAsnPheIleArgPheLeuGlnProTyrAsnAlaSerHisLeu

541 TACGTCTGTGGCACCTACGCCTTCCAGCCCAAGTGCACCTACGTC
    TyrValCysGlyThrTyrAlaPheGlnProLysCysThrTyrVal

586 AACATGCTCACCTTCACTTTGGAGCATGGAGAGTTTGAAGATGGG
    AsnMetLeuThrPheThrLeuGluHisGlyGluPheGluAspGly

631 AAGGGCAAGTGTCCCTATGACCCAGCTAAGGGCCATGCTGGCCTT
    LysGlyLysCysProTyrAspProAlaLysGlyHisAlaGlyLeu

676 CTTGTGGATGGTGAGCTGTACTCGGCCACACTCAACAACTTCCTG
    LeuValAspGlyGluLeuTyrSerAlaThrLeuAsnAsnPheLeu

721 GGCACGGAACCCATTATCCTGCGTAACATGGGGCCCCACCACTCC
    GlyThrGluProIleIleLeuArgAsnMetGlyProHisHisSer
```

Fig. 6

```
766 ATGAAGACAGAGTACCTGGCCTTTTGGCTCAACGAACCTCACTTT
    MetLysThrGluTyrLeuAlaPheTrpLeuAsnGluProHisPhe

811 GTAGGCTCTGCCTATGTACCTGAGAGGGTGGGCCTGCTGTGGACA
    ValGlySerAlaTyrValProGluArgValGlyLeuLeuTrpThr

856 ATGGCATACTCTCTTCCAGCCCTAGGAGGAGGGCTCCTAACAGTG
    MetAlaTyrSerLeuProAlaLeuGlyGlyGlyLeuLeuThrVal

901 TAACTTATTGTGTCCCCGCGTATTTATTTGTTGTAAATATTTGAG
946 TATTTTTATATTGACAAATAAA
```

Fig. 6 (continued)

```
  1  GGCACCAGGCCTTCCGGAGAGACGCAGTCGGCTGCCACCCCGGGA
                                                 M

 46  TGGGTCGCTGGTGCCAGACCGTCGCGCGGGCAGCGCCCCCGGA
     etGlyArgTrpCysGlnThrValAlaArgGlyGlnArgProArgT

 91  CGTCTGCCCCCTCCCGCGCCGGTGCCCTGCTGCTGCTGCTTCTGT
     hrSerAlaProSerArgAlaGlyAlaLeuLeuLeuLeuLeuLeuL

136  TGCTGAGGTCTGCAGGTTGCTGGGGCGCAGGGGAAGCCCCGGGGG
     euLeuArgSerAlaGlyCysTrpGlyAlaGlyGluAlaProGlyA

181  CGCTGTCCACTGCTGATCCCGCCGACCAGAGCGTCCAGTGTGTCC
     laLeuSerThrAlaAspProAlaAspGlnSerValGlnCysValP

226  CCAAGGCCACCTGTCCTTCCAGCCGGCCTCGCCTTCTCTGGCAGA
     roLysAlaThrCysProSerSerArgProArgLeuLeuTrpGlnT

271  CCCCGACCACCCAGACACTGCCCTCGACCACCATGGAGACCCAAT
     hrProThrThrGlnThrLeuProSerThrThrMetGluThrGlnP

316  TCCCAGTTTCTGAAGGCAAAGTCGACCCATACCGCTCCTGTGGCT
     heProValSerGluGlyLysValAspProTyrArgSerCysGlyP

361  TTTCCTACGAGCAGGACCCCACCCTCAGGGACCCAGAAGCCGTGG
     heSerTyrGluGlnAspProThrLeuArgAspProGluAlaValA

406  CTCGGCGGTGGCCCTGGATGGTCAGCGTGCGGGCCAATGGCACAC
     laArgArgTrpProTrpMetValSerValArgAlaAsnGlyThrH

451  ACATCTGTGCCGGCACCATCATTGCCTCCCAGTGGGTGCTGACTG
     isIleCysAlaGlyThrIleIleAlaSerGlnTrpValLeuThrV

496  TGGCCCACTGCCTGATCTGGCGTGATGTTATCTACTCAGTGAGGG
     alAlaHisCysLeuIleTrpArgAspValIleTyrSerValArgV

541  TGGGGAGTCCGTGGATTGACCAGATGACGCAGACCGCCTCCGATG
     alGlySerProTrpIleAspGlnMetThrGlnThrAlaSerAspV

586  TCCCGGTGCTCCAGGTCATCATGCATAGCAGGTACCGGGCCCAGC
     alProValLeuGlnValIleMetHisSerArgTyrArgAlaGlnA

631  GGTTCTGGTCCTGGGTGGGCCAGGCCAACGACATCGGCCTCCTCA
     rgPheTrpSerTrpValGlyGlnAlaAsnAspIleGlyLeuLeuL

676  AGCTCAAGCAGGAACTCAAGTACAGCAATTACGTGCGGCCCATCT
     ysLeuLysGlnGluLeuLysTyrSerAsnTyrValArgProIleC
```

Fig. 7

721 GCCTGCCTGGCACGGACTATGTGTTGAAGGACCATTCCCGCTGCA
ysLeuProGlyThrAspTyrValLeuLysAspHisSerArgCysT

766 CTGTGACGGGCTGGGGACTTTCCAAGGCTGACGGCATGTGGCCTC
hrValThrGlyTrpGlyLeuSerLysAlaAspGlyMetTrpProG

811 AGTTCCGGACCATTCAGGAGAAGGAAGTCATCATCCTGAACAACA
lnPheArgThrIleGlnGluLysGluValIleIleLeuAsnAsnL

856 AAGAGTGTGACAATTTCTACCACAACTTCACCAAAATCCCCACTC
ysGluCysAspAsnPheTyrHisAsnPheThrLysIleProThrL

901 TGGTTCAGATCATCAAGTCCCAGATGATGTGTGCGGAGGACACCC
euValGlnIleIleLysSerGlnMetMetCysAlaGluAspThrH

946 ACAGGGAGAAGTTCTGCTATGAGCTAACTGGAGAGCCCTTGGTCT
isArgGluLysPheCysTyrGluLeuThrGlyGluProLeuValC

991 GCTCCATGGAGGGCACGTGGTACCTGGTGGGATTGGTGAGCTGGG
ysSerMetGluGlyThrTrpTyrLeuValGlyLeuValSerTrpG

1036 GTGCAGGCTGCCAGAAGAGCGAGGCCCCACCCATCTACCTACAGG
lyAlaGlyCysGlnLysSerGluAlaProProIleTyrLeuGlnV

1081 TCTCCTCCTACCAACACTGGATCTGGGACTGCCTCAACGGGCAGG
alSerSerTyrGlnHisTrpIleTrpAspCysLeuAsnGlyGlnA

1126 CCCTGGCCCTGCCAGCCCCATCCAGGACCCTGCTCCTGGCACTCC
laLeuAlaLeuProAlaProSerArgThrLeuLeuLeuAlaLeuP

1171 CACTGCCCCTCAGCCTCCTTGCTGCCCTCTGACTCTGTGTGCCCT
roLeuProLeuSerLeuLeuAlaAlaLeu

1216 CCCTCACTTGTGGGCCCCCCTTGCCTCCGTGCCCAGGTTGCTGTG
1261 GGTGCAGCTGTCACAGCCCTGAGAGTCAGGGTGGAGATGAGGTGC
1306 TCAATTAAACATTACTGTTTTCCATGTAAAAAAAAAAAAAAAAAA
1351 AAAAAAAAA

Fig. 7 (continued)

CACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCCCCTTTGGAGCCTCCTGCTGGCCACTGGCTGGGATCAGGACACC
81
AGTGATGGTAAGTGCTGGCCCAGACTGAAGCTCGGAGAGGCACTCTGCTTGCCCAGCGTCACAGTCTTAGCTCCCAACTG
161
TCCTGGCTTCCAGTCTCCCTTGCTTCCCAGATCCCAGACTCTAGCCCCAGCCCCGTCTCTTTCACCAGCTCCTGGACCC
241
TACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAACTGTATCTACAACCAGCTGCACCAGCGACACCTGTCC
321
AACCCGGCCCGGCCTGGGATGCTATGTGGGGGCCCCCAGCCTGGGGTGCAGGGCCCCTGTCAGGTCTGATAGGGAGAAGA
401
GAAGGAGCAGAAGGGGAGGGGCCTAACCCTGGGCTGGGGGTTGGACTCACAGGACTGGGGGAAAGAGCTGCAATCAGAGG
481
GTGTCTGCCATAGCTGGGCTCAGGCATCTGTCCTTGGCTTTGTTGCCTGGCTCCAGGGAGATTCCGGGGGCCCTGTGCTG
561
TGCCTCGAGCCTGACGGACACTGGGTTCAGGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTGT
641
GCTGCTGACCAACACAGCTGCTCACAGTTCCTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTTTCCTGGCCCAGAGCCCAG
721
AGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGATCCTTGAGGACAGCAGGTCCCCAGGCAGGAGCACCC
MetSerAspGluAspSerCysValAlaCysGlySerLeuArgThrAlaGlyProGlnAlaGlyAlaPro
801
TCCCCATGGCCCTGGGAGGCCAGGCTGATGCACCAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTCAGAGGAGGCGGT
SerProTrpProTrpGluAlaArgLeuMetHisGlnGlyGlnLeuAlaCysGlyGlyAlaLeuValSerGluGluAlaVa
881
GCTAACTGCTGCCCACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGACCGGAGGAGT
lLeuThrAlaAlaHisCysPheIleGlyArgGlnAlaProGluGluTrpSerValGlyLeuGlyThrArgProGluGluT
961
GGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGGCTACGACATGGCCCTCCTGCTGCTGGCC
rpGlyLeuLysGlnLeuIleLeuHisGlyAlaTyrThrHisProGluGlyGlyTyrAspMetAlaLeuLeuLeuLeuAla
1041
CAGCCTGTGACACTGGGAGCCAGCCTGCGGCCCCTCTGCCTGCCCTATGCTGACCACCACCTGCCTGATGGGGAGCGTGG
GlnProValThrLeuGlyAlaSerLeuArgProLeuCysLeuProTyrAlaAspHisHisLeuProAspGlyGluArgGl
1121
CTGGGTTCTGGGACGGGCCCGCCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCTCCTGGGGCCTAGGG
yTrpValLeuGlyArgAlaArgProGlyAlaGlyIleSerSerLeuGlnThrValProValThrLeuLeuGlyProArgA
1201
CCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCGGGGATGGTGTGTACCAGTGCTGTGGGT
laCysSerArgLeuHisAlaAlaProGlyGlyAspGlySerProIleLeuProGlyMetValCysThrSerAlaValGly
1281
GAGCTGCCCAGCTGTGAGGTGAGCCCCAGGCCCCCACACCTTACCTAACAGGCCCCTGGCATCCCCTCACCCAATAGCTC
GluLeuProSerCysGluValSerProArgProProHisLeuThr
1361
AAGAACGGACCTTCCAGGCTTGGCCTCTGGACCCACCTCCCACCTGAAGCTAAGCCTTTTTGCCAATTAGCCCCCAAACA
1441
GCCAG

Fig. 8

1 CTTAACAGCCACTTGTTTCATCCCACCTGGGCATTAGGTTGACTT

46 CAAAGATGCCTCAGTTACTGCAAAACATTAATGGGATCATCGAGG
MetProGlnLeuLeuGlnAsnIleAsnGlyIleIleGluA

91 CCTTCAGGCGCTATGCAAGGACGGAGGGCAACTGCACAGCGCTCA
laPheArgArgTyrAlaArgThrGluGlyAsnCysThrAlaLeuT

136 CCCGAGGGGAGCTGAAAAGACTCTTGGAGCAAGAGTTTGCCGATG
hrArgGlyGluLeuLysArgLeuLeuGluGlnGluPheAlaAspV

181 TGATTGTGAAACCCCACGATCCAGCAACTGTGGATGAGGTCCTGC
alIleValLysProHisAspProAlaThrValAspGluValLeuA

226 GTCTGCTGGATGAAGACCACACAGGGACTGTGGAATTCAAGGAAT
rgLeuLeuAspGluAspHisThrGlyThrValGluPheLysGluP

271 TCCTGGTCTTAGTGTTTAAAGTTGCCCAGGCCTGTTTCAAGACAC
heLeuValLeuValPheLysValAlaGlnAlaCysPheLysThrL

316 TGAGCGAGAGTGCTGAGGGAGCCTGCGGCTCTCAAGAGTCTGGAA
euSerGluSerAlaGluGlyAlaCysGlySerGlnGluSerGlyS

361 GCCTCCACTCTGGGGCCTCGCAGGAGCTGGGCGAAGGACAGAGAA
erLeuHisSerGlyAlaSerGlnGluLeuGlyGluGlyGlnArgS

406 GTGGCACTGAAGTGGGAAGGGCGGGGAAAGGGCAGCATTATGAGG
erGlyThrGluValGlyArgAlaGlyLysGlyGlnHisTyrGluG

451 GGAGCAGCCACAGACAGAGCCAGCAGGGTTCCAGAGGGCAGAACA
lySerSerHisArgGlnSerGlnGlnGlySerArgGlyGlnAsnA

496 GGCCTGGGGTTCAGACCCAGGGTCAGGCCACTGGCTCTGCGTGGG
rgProGlyValGlnThrGlnGlyGlnAlaThrGlySerAlaTrpV

541 TCAGCAGCTATGACAGGCAAGCTGAGTCCCAGAGCCAGGAAAGAA
alSerSerTyrAspArgGlnAlaGluSerGlnSerGlnGluArgI

586 TAAGCCCGCAGATACAACTCTCTGGGCAGACAGAGCAGACCCAGA
leSerProGlnIleGlnLeuSerGlyGlnThrGluGlnThrGlnL

631 AAGCTGGAGAAGGCAAGAGGAATCAGACAACAGAGATGAGGCCAG
ysAlaGlyGluGlyLysArgAsnGlnThrThrGluMetArgProG

676 AGAGACAGCCACAGACCAGGGAACAGGACAGAGCCCACCAGACAG
luArgGlnProGlnThrArgGluGlnAspArgAlaHisGlnThrG

Fig. 9

721 GTGAGACTGTGACTGGATCTGGAACTCAGACCCAGGCAGGTGCCA
lyGluThrValThrGlySerGlyThrGlnThrGlnAlaGlyAlaT

766 CCCAGACTGTGGAGCAGGACAGCAGCCACCAGACAGGAAGCACCA
hrGlnThrValGluGlnAspSerSerHisGlnThrGlySerThrS

811 GCACCCAGACACAGGAGTCCACCAATGGCCAGAACAGAGGGACTG
erThrGlnThrGlnGluSerThrAsnGlyGlnAsnArgGlyThrG

856 AGATCCACGGTCAAGGCAGGAGCCAGACCAGCCAGGCTGTGACAG
luIleHisGlyGlnGlyArgSerGlnThrSerGlnAlaValThrG

901 GAGGACACACTCAGATACAGGCAGGGTCACACACCGAGACTGTGG
lyGlyHisThrGlnIleGlnAlaGlySerHisThrGluThrValG

946 AGCAGGACAGAAGCCAAACTGTAAGCCACGGAGGGGCTAGAGAAC
luGlnAspArgSerGlnThrValSerHisGlyGlyAlaArgGluG

991 AGGGACAGACCCAGACGCAGCCAGGCAGTGGTCAAAGATGGATGC
lnGlyGlnThrGlnThrGlnProGlySerGlyGlnArgTrpMetG

1036 AAGTGAGCAACCCTGAGGCAGGAGAGACAGTACCGGGAGGACAGG
lnValSerAsnProGluAlaGlyGluThrValProGlyGlyGlnA

1081 CCCAGACTGGGGCAAGCACTGAGTCAGGAAGGCAGGAGTGGAGCA
laGlnThrGlyAlaSerThrGluSerGlyArgGlnGluTrpSerS

1126 GCACTCACCCAAGGCGCTGTGTGACAGAAGGGCAGGGAGACAGAC
erThrHisProArgArgCysValThrGluGlyGlnGlyAspArgG

1171 AGCCCACAGTGGTTGGTGAGGAATGGGTTGATGACCACTCAAGGG
lnProThrValValGlyGluGluTrpValAspAspHisSerArgG

1216 AGACAGTGATCCTCAGGCTGGACCAGGGCAACTTGCATACCAGTG
luThrValIleLeuArgLeuAspGlnGlyAsnLeuHisThrSerV

1261 TTTCCTCAGCACAGGGCCAGGATGCAGCCCAGTCAGAAGAGAAGC
alSerSerAlaGlnGlyGlnAspAlaAlaGlnSerGluGluLysA

1306 GAGGCATCACAGCTAGAGAGCTGTATTCCTACTTGAGAAGCACCA
rgGlyIleThrAlaArgGluLeuTyrSerTyrLeuArgSerThrL

1351 AGCCATGACTTCCCCGACTCCAATGTCCAGTACTGGAAGAAGACA
ysPro

1396 GCTGGAGAGAGTTTGGCTTGTCCTGCATGGCCAATCCAGTGGGTG
1441 CATCCCTGGACATCAGCTCTTCATTATGCAGCTTCCCTTTTAGGT
1486 CTTTCTCAATGAGATAATTTCTGCAAGGAGCTTTCTATCCTGAAC
1531 TCTTCTTTCTTACCTGCTTTGCGGTGCAGACCCTCTCAGGAGCAG
1576 GAAGACTCAGAACAAGTCACCCCTT

Fig. 9 (continued)

1. 11618130.0.184_Cura_108
2. 11618130.0.27_Cura_56

```
116181300184_cura_108 MSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGR
11618130027_cura_56   MSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFNGR

116181300184_cura_108 QAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYA
11618130027_cura_56   QAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRALCLPYF

116181300184_cura_108 DHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGMVCTS
11618130027_cura_56   DHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGMVCTS

116181300184_cura_108 AVGELPSCEVSPRPPHLT~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
11618130027_cura_56   AVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVSSLDW

116181300184_cura_108 ~~~~~~~~~~~~~~~~~~~~~~~~~~~
11618130027_cura_56   QVYFAEEPEPEAEPGSCLANISQPTSC
```

Fig. 10

Sequences analyzed:

1. 14578444-0-47_Cura_56
2. 14578444-0-143Cura_56

```
14578444047_cura_56    MEKMLAGCFLLILGQIVLLPCEARERSRGRSISRGRHARTHPQTALLESSCENKRADLVF
145784440143_cura_56   MEKMLAGCFLLILGQIVLLPAEARERSRGRSISRGRHARTHPQTALLESSCENKRADLVF

14578444047_cura_56    IIDSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEV
145784440143_cura_56   IIDSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEV

14578444047_cura_56    ERAVKRMRHLSTGTMTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEV
145784440143_cura_56   ERAVKRMRHLSTGTMTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEV

14578444047_cura_56    AAKARDTGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAH
145784440143_cura_56   AAKARDTGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAH

14578444047_cura_56    MCSTLEHNCAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGS
145784440143_cura_56   MCSTLEHNCAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGS

14578444047_cura_56    FVCECYSGYALAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCT
145784440143_cura_56   FVCECYSGYALAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCT
```

Fig. 11

```
14578444047_cura_56   KIDYCASSNHGCQYECVNTDDSYSCHCLKGFTLNPDKKTCRRINYCALNKPGCEHECVNM
145784440143_cura_56  KIDYCASSNHGCQYECVNTDDSYSCHCLKGFTLNPDKKTCRRINYCALNKPGCEHECVNM

14578444047_cura_56   EESYYCRCHRGYTLDPNGKPCSRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLINEDLK
145784440143_cura_56  EESYYCRCHRGYTLDPNGKPCSRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLINEDLK

14578444047_cura_56   TCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSDGKTCAKLDSCALGDHGCEHSC
145784440143_cura_56  TCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSDGKTCAKLDSCALGDHGCEHSC

14578444047_cura_56   VSSEDSFVCQCFEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLTE
145784440143_cura_56  VSSEDSFVCQCFEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLTE

14578444047_cura_56   DGKRCRISSGKDVCKSTHHGCEHICVNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLV
145784440143_cura_56  DGKRCRISSGKDVCKSTHHGCEHICVNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLV

14578444047_cura_56   FVIDGSKSLGEENFEVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKD
145784440143_cura_56  FVIDGSKSLGEENFEVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKD

14578444047_cura_56   MKKAVAHMKYMGKGSMTGLALKHMFERSFTQGEGARPFSTRVPRAAIVFTDGRAQDDVSE
145784440143_cura_56  MKKAVAHMKYMGKGSMTGLALKHMFERSFTQGEGARPLFHKGAQSSHCVHRRTGSG~~~~

14578444047_cura_56   WASKAKANGITMYAVGVGKAIEEELQEIASEPTNKHLFYAEDFSTMDEISEKLKKGICEA
145784440143_cura_56  ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

14578444047_cura_56   LEDSDGRQDSPAGELPKTVQQPTESEPVTINIQDLLSCSNFAVQHRYLFEEDNLLRSTQK
145784440143_cura_56  ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

14578444047_cura_56   LSHSTKPSGSPLEEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR
145784440143_cura_56  ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
```

Fig. 11 (continued)

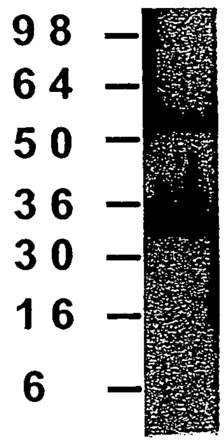

Fig. 12

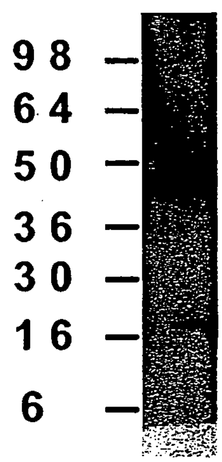

Fig. 13

Normal & Tumor Tissues	11696905	16406477.0.206	21433858	21637262.0.64
Endothelial cells	3.5	0.0	6.6	0.0
Endothelial cells (treated)	2.9	0.0	2.0	0.0
Pancreas	9.4	3.1	1.2	0.0
Pancreatic ca. CAPAN 2	3.7	0.0	0.3	0.0
Adipose	60.7	0.3	22.5	0.8
Adrenal gland	18.0	0.0	3.2	0.2
Thyroid	13.8	0.0	4.6	2.4
Salivary gland	0.0	0.6	0.7	36.3
Pituitary gland	2.2	0.6	4.0	1.4
Brain (fetal)	3.1	0.5	6.9	0.7
Brain (whole)	4.4	0.7	24.5	0.3
Brain (amygdala)	17.2	0.1	5.0	0.4
Brain (cerebellum)	1.6	1.2	41.8	1.4
Brain (hippocampus)	9.3	0.8	10.4	0.6
Brain (hypothalamus)	5.7	10.0	2.3	0.5
Brain (substantia nigra)	33.2	0.7	5.2	0.1
Brain (thalamus)	22.7	0.5	5.2	0.0
Spinal cord	21.8	0.3	4.0	1.5
CNS ca. (glio/astro) U87-MG	2.2	0.0	1.0	0.0
CNS ca. (glio/astro) U-118-MG	4.5	0.0	1.5	0.0
CNS ca. (astro) SW1783	0.0	0.0	0.7	0.0
CNS ca.* (neuro; met) SK-N-AS	2.7	0.0	12.6	0.1
CNS ca. (astro) SF-539	0.2	0.0	0.0	0.0
CNS ca. (astro) SNB-75	1.3	0.0	0.6	0.0
CNS ca. (glio) SNB-19	0.6	0.0	0.8	0.2
CNS ca. (glio) U251	0.2	0.0	3.6	0.1
CNS ca. (glio) SF-295	6.2	0.1	0.2	0.0
Heart	10.7	0.1	1.3	0.1
Skeletal muscle	18.4	0.0	0.2	0.2
Bone marrow	11.1	0.0	0.1	0.0
Thymus	7.3	0.9	2.5	0.5
Spleen	2.9	0.1	1.4	0.0
Lymph node	4.3	0.1	1.3	0.1

Fig. 14

Normal & Tumor Tissues	11696905	16406477.0.206	21433858	21637262.0.64
Colon (ascending)	1.3	0.2	5.1	1.3
Stomach	5.4	0.2	5.7	0.0
Small intestine	7.0	0.2	1.7	0.0
Colon ca. SW480	0.4	0.0	0.0	0.1
Colon ca.* (SW480 met)SW620	0.1	0.0	0.0	0.0
Colon ca. HT29	0.4	0.0	0.0	0.1
Colon ca. HCT-116	4.4	0.0	0.0	0.0
Colon ca. CaCo-2	1.1	0.1	0.1	0.0
Colon ca. HCT-15	11.0	0.2	0.3	0.2
Colon ca. HCC-2998	0.0	0.0	1.3	0.0
Gastric ca.* (liver met) NCI-N87	4.9	0.3	1.9	0.0
Bladder	18.8	0.1	10.8	0.1
Trachea	4.8	0.0	2.2	100.0
Kidney	7.3	0.4	13.1	0.1
Kidney (fetal)	11.0	1.8	29.5	0.1
Renal ca. 786-0	0.4	0.0	0.0	0.0
Renal ca. A498	56.3	0.0	0.0	0.1
Renal ca. RXF 393	2.7	0.0	0.1	0.0
Renal ca. ACHN	1.0	0.0	0.1	0.1
Renal ca. UO-31	1.8	0.0	0.4	0.1
Renal ca. TK-10	13.4	0.5	0.2	0.1
Liver	74.7	0.7	2.1	0.1
Liver (fetal)	27.7	1.2	0.9	0.0
Liver ca. (hepatoblast HepG2	7.4	0.0	0.0	0.0
Lung	9.9	0.0	2.9	0.0
Lung (fetal)	1.5	1.5	3.0	0.0
Lung ca. (small cell) LX-1	0.4	0.0	0.0	0.0
Lung ca. (small cell) NCI-H69	0.5	0.1	9.3	0.5
Lung ca. (s.cell var.) SHP-77	0.6	0.4	100.0	1.7
Lung ca. (large cell) NCI-H460	20.6	0.3	66.9	0.6
Lung ca. (non-sm. cell) A549	3.3	0.0	15.5	0.1
Lung ca. (non-s.cell) NCI-H23	7.4	0.5	9.0	0.0
Lung ca (non-s.cell) HOP-62	32.1	0.1	1.5	0.1
Lung ca. (non-s.cl) NCI-H522	11.0	0.6	0.0	0.0
Lung ca. (squam.) SW 900	3.3	0.9	6.1	0.1

Fig. 14 (continued)

Normal & Tumor Tissues	11696905.0	16406477.0.206	21433858.0	21637262.0.64
Mammary gland	30.4	1.5	12.2	0.0
Breast ca.* (pl. effusion) MCF-7	4.8	0.0	0.0	0.0
Breast ca.* (pl.ef) MDA-MB-231	2.2	0.0	0.0	0.1
Breast ca.* (pl. effusion) T47D	9.8	0.1	0.9	0.6
Breast ca. BT-549	9.2	0.1	1.2	0.3
Breast ca. MDA-N	1.3	0.0	0.0	0.0
Ovary	6.0	0.3	9.7	0.0
Ovarian ca. OVCAR-3	1.6	0.1	0.8	0.1
Ovarian ca. OVCAR-4	1.9	0.0	0.0	0.0
Ovarian ca. OVCAR-5	7.1	0.3	6.9	0.6
Ovarian ca. OVCAR-8	1.3	2.7	2.7	0.0
Ovarian ca. IGROV-1	0.7	0.2	5.0	0.0
Ovarian ca.* (ascites) SK-OV-3	2.5	0.0	0.2	0.0
Myometrium	2.3	0.0	41.2	1.2
Uterus	6.3	0.6	25.7	0.1
Placenta	100.0	0.0	94.0	0.1
Prostate	13.3	0.1	3.4	0.1
Prostate ca.* (bone met) PC-3	7.9	1.7	0.2	0.2
Testis	14.3	100.0	37.1	4.0
Melanoma Hs688(A).T	1.4	0.0	0.0	0.0
Melanoma* (met) Hs688(B).T	5.3	0.0	0.0	0.0
Melanoma UACC-62	0.6	0.0	0.0	0.0
Melanoma M14	0.9	0.1	0.3	0.2
Melanoma LOX IMVI	1.0	0.0	0.0	0.1
Melanoma* (met) SK-MEL-5	0.0	0.0	8.7	0.0
Melanoma SK-MEL-28	100.0	0.0	0.0	0.0

Fig. 14 (continued)

Drawings

Figure 15. Nucleotide Sequence for CG106318-01.

>CG106318-01 4810 nt
GTCCATGGGGCCGATGTATGGGAGATGAATGTGGTCCCGGAGGCATCCAAACGAGGGCTG
TGTGGTGTGCTCATGTGGAGGGATGGACTACACTGCATACTAACTGTAAGCAGGCCGAGA
GACCCAATAACCAGCAGAATTGTTTCAAAGTTTGCGATTGGCACAAAGAGTTGTACGACT
GGAGACTGGGACCTTGGAATCAGTGTCAGCCCGTGATTTCAAAAAGCCTAGAGAAACCTC
TTGAGTGCATTAAGGGGGAAGAAGGTATTCAGGTGAGGGAGATAGCGTGCATCCAGAAAG
ACAAAGACATTCCTGCGGAGGATATCATCTGTGAGTACTTTGAGCCCAAGCCTCTCCTGG
AGCAGGCTTGCCTCATTCCTTGCCAGCAAGATTGCATCGTGTCTGAATTTTCTGCCTGGT
CCGAATGCTCCAAGACCTGCGGCAGCGGGCTCCAGCACCGGACGCGTCATGTGGTGGCGC
CCCCGCAGTTCGGAGGCTCTGGCTGTCCAAACCTGACGGAGTTCCAGGTGTGCCAATCCA
GTCCATGCGAGGCCGAGGAGCTCAGGTACAGCCTGCATGTGGGGCCCTGGAGCACCTGCT
CAATGCCCCACTCCCGACAAGTAAGACAAGCAAGGAGACGCGGGAAGAATAAAGAACGGG
AAAAGGACCGCAGCAAAGGAGTAAAGGATCCAGAAGCCCGCGAGCTTATTAAGAAAAAGA
GAAACAGAAACAGGCAGAACAGACAAGAGAACAAATATTGGGACATCCAGATTGGATATC
AGACCAGAGAGGTTATGTGCATTAACAAGACGGGGAAAGCTGCTGATTTAAGCTTTTGCC
AGCAAGAGAAGCTTCCAATGACCTTCCAGTCCTGTGTGATCACCAAAGAGTGCCAGGTTT
CCGAGTGGTCAGAGTGGAGCCCCTGCTCAAAAACATGCCATGACATGGTGTCCCCTGCAG
GCACTCGTGTAAGGACACGAACCATCAGGCAGTTTCCCATTGGCAGTGAAAAGGAGTGTC
CAGAATTTGAAGAAAAAGAACCCTGTTTGTCTCAAGGAGATGGAGTTGTCCCCTGTGCCA
CGTATGGCTGGAGAACTACAGAGTGGACTGAGTGCCGTGTGGACCCTTTGCTCAGTCAGC
AGGACAAGAGGCGCGGCAACCAGACGGCCCTCTGTGGAGGGGGCATCCAGACCCGAGAGG
TGTACTGCGTGCAGGCCAACGAAAACCTCCTCTCACAATTAAGTACCCACAAGAACAAAG
AAGCCTCAAAGCCAATGGACTTAAAATTATGCACTGGACCTATCCCTAATACTACACAGC
TGTGCCACATTCCTTGTCCAACTGAATGTGAAGTTTCACCTTGGTCAGCTTGGGGACCTT
GTACTTATGAAAACTGTAATGATCAGCAAGGGAAAAAAGGCTTCAAACTGAGGAAGCGGC
GCATTACCAATGAGCCCACTGGAGGCTCTGGGGTAACCGGAAACTGCCCTCACTTACTGG
AAGCCATTCCCTGTGAAGAGCCTGCCTGTTATGACTGGAAAGCGGTGAGACTGGGAGACT
GCGAGCCAGATAACGGAAAGGAGTGTGGTCCAGGCACGCAAGTTCAAGAGGTTGTGTGCA
TCAACAGTGATGGAGAAGAAGTTGACAGACAGCTGTGCAGAGATGCCATCTTCCCCATCC
CTGTGGCCTGTGATGCCCCATGCCCGAAAGACTGTGTGCTCAGCACATGGTCTACGTGGT
CCTCCTGCTCACACACCTGCTCAGGGAAAACGACAGAAGGGAAACAGATACGAGCACGAT
CCATTCTGGCCTATGCGGGTGAAGAAGGTGGAATTCGCTGTCCAAATAGCAGTGCTTTGC
AAGAAGTACGAAGCTGTAATGAGCATCCTTGCACAGTGTACCACTGGCAAACTGGTCCCT
GGGGCCAGTGCATTGAGGACACCTCAGTATCGTCCTTCAACACAACTACGACTTGGAATG
GGGAGGCCTCCTGCTCTGTCGGCATGCAGACAAGAAAAGTCATCTGTGTGCGAGTCAATG
TGGGCCAAGTGGGACCCAAAAAATGTCCTGAAAGCCTTCGACCTGAAACTGTAAGGCCTT
GTCTGCTTCCTTGTAAGAAGGACTGTATTGTGACCCCATATAGTGACTGGACATCATGCC
CCTCTTCGTGTAAAGAAGGGGACTCCAGTATCAGGAAGCAGTCTAGGCATCGGGTCATCA
TTCAGCTGCCAGCCAACGGGGGCCGAGACTGCACAGATCCCCTCTATGAAGAGAAGGCCT
GTGAGGCACCTCAAGCGTGCCAAAGCTACAGGTGGAAGACTCACAAATGGCGCAGATGCC
AATTAGTCCCTTGGAGCGTGCAACAAGACAGCCCTGGAGCACAGGAAGGCTGTGGGCCTG
GGCGACAGGCAAGAGCCATTACTTGTCGCAAGCAAGATGGAGGACAGGCTGGAATCCATG
AGTGCCTACAGTATGCAGGCCCTGTGCCAGCCCTTACCCAGGCCTGCCAGATCCCCTGCC
AGGATGACTGTCAATTGACCAGCTGGTCCAAGTTTTCTTCATGCAATGGAGACTGTGGTG
CAGTTAGGACCAGAAAGCGCACTCTTGTTGGAAAAAGTAAAAAGAAGGAAAAATGTAAAA
ATTCCCATTTGTATCCCCTGATTGAGACTCAGTATTGTCCTTGTGACAAATATAATGCAC
AACCTGTGGGGAACTGGTCAGACTGTATTTTACCAGAGGGAAAAGTGGAAGTGTTGCTGG
GAATGAAAGTACAAGGAGACATCAAGGAATGCGGACAAGGATATCGTTACCAAGCAATGG
CATGCTACGATCAAAATGGCAGGCTTGTGGAAACATCTAGATGTAACAGCCATGGTTACA
TTGAGGAGGCCTGCATCATCCCCTGCCCCTCAGACTGCAAGCTCAGTGAGTGGTCCAACT
GGTCGCGCTGCAGCAAGTCCTGTGGGAGTGGTGTGAAGGTTCGTTCTAAATGGCTGCGTG
AAAAACCATATAATGGAGGAAGGCCTTGCCCCAAACTGGACCATGTCAACCAGGCACAGG
TGTATGAGGTTGTCCCATGCCACAGTGACTGCAACCAGTACCTATGGGTCACAGAGCCCT
GGAGCATCTGCAAGGTGACCTTTGTGAATATGCGGGAGAACTGTGGAGAGGGCGTGCAAA
CCCGAAAAGTGAGATGCATGCAGAATACAGCAGATGGCCCTTCTGAACATGTAGAGGATT
ACCTCTGTGACCCAGAAGAGATGCCCCTGGGCTCTAGAGTGTGCAAATTACCATGCCCTG
AGGACTGTGTGATATCTGAATGGGGTCCATGGACCCAATGTGTTTTGCCTTGCAATCAAA
GCAGTTTCCGGCAAAGGTCAGCTGATCCCATCAGACAACCAGCTGATGAAGGAAGATCTT
GCCCTAATGCTGTTGAGAAAGAACCCTGTAACCTGAACAAAAACTGCTACCACTATGATT
ATAATGTAACAGACTGGAGTACATGTCAGCTGAGTGAGAAGGCAGTTTGTGGAAATGGAA
TAAAAACAAGGATGTTGGATTGTGTTCGAAGTGATGGCAAGTCAGTTGACCTGAAATATT

GTGAAGCGCTTGGCTTGGAGAAGAACTGGCAGATGAACACGTCCTGCATGGTGGAATGCC
CTGTGAACTGTCAGCTTTCTGATTGGTCTCCTTGGTCAGAATGTTCTCAAACATGTGGCC
TCACAGGAAAAATGATCCGAAGACGAACAGTGACCCAGCCCTTTCAAGGTGATGGAAGAC
CATGCCCTTCCCTGATGGACCAGTCCAAACCCTGCCCAGTGAAGCCTTGTTATCGGTGGC
AATATGGCCAGTGGTCTCCATGCCAAGTGCAGGAGGCCCAGTGTGGAGAAGGGACCAGAA
CAAGGAACATTTCTTGTGTAGTAAGTGATGGGTCAGCTGATGATTTCAGCAAAGTGGTGG
ATGAGGAATTCTGTGCTGACATTGAACTCATTATAGATGGTAATAAAAATATGGTTCTGG
AGGAATCCTGCAGCCAGCCTTGCCCAGGTGACTGTTATTTGAAGGACTGGTCTTCCTGGA
GCCTGTGTCAGCTGACCTGTGTGAATGGTGAGGATCTAGGCTTTGGTGGAATACAGGTCA
GATCCAGACCGGTGATTATACAAGAACTAGAGAATCAGCATCTGTGCCCAGAGCAGATGT
TAGAAACAAAATCATGTTATGATGGACAGTGCTATGAATATAAATGGATGGCCAGTGCTT
GGAAGGGCTCTTCCCGAACAGTGTGGTGTCAAAGGTCAGATGGTATAAATGTAACAGGGG
GCTGCTTGGTGATGAGCCAGCCTGATGCCGACAGGTCTTGTAACCCACCGTGTAGTCAAC
CCCACTCGTACTGTAGCGAGACAAAAACATGCCATTGTGAAGAAGGGTACACTGAAGTCA
TGTCTTCTAACAGCACCCTTGAGCAATGCACACTTATCCCCGTGGTGGTATTACCCACCA
TGGAGGACAAAAGAGGAGATGTGAAAACCAGTCGGGCTGTACATCCAACCCAACCCTCCA
GTAACCCAGCAGGACGGGGAAGGACCTGGTTTCTACAGCCATTTGGGCCAGATGGGAGAC
TAAAGACCTGGGTTTACGGTGTAGCAGCTGGGGCATTTGTGTTACTCATCTTTATTGTCT
CCATGATTTATCTAGCTTGCAAAAAGCCAAAGAAACCCCAAAGAAGGCAAAACAACCGAC
TGAAACCTTTAACCTTAGCCTATGATGGAGATGCCGACATGTAACATATAACTTTTCCTG
GCAACAACCA (SEQ ID NO: 40)

Protein Sequence for CG106318-01 ORF Start: 18 ORF Stop: 4782 Frame: 3

Protein Sequence:

>CG106318-01-prot 1588 aa
MGDECGPGGIQTRAVWCAHVEGWTTLHTNCKQAERPNNQQNCFKVCDWHKELYDWRLGPW
NQCQPVISKSLEKPLECIKGEEGIQVREIACIQKDKDIPAEDIICEYFEPKPLLEQACLI
PCQQDCIVSEFSAWSECSKTCGSGLQHRTRHVVAPPQFGGSGCPNLTEFQVCQSSPCEAE
ELRYSLHVGPWSTCSMPHSRQVRQARRRGKNKEREKDRSKGVKDPEARELIKKKRNRNRQ
NRQENKYWDIQIGYQTREVMCINKTGKAADLSFCQQEKLPMTFQSCVITKECQVSEWSEW
SPCSKTCHDMVSPAGTRVRTRTIRQFPIGSEKECPEFEEKEPCLSQGDGVVPCATYGWRT
TEWTECRVDPLLSQQDKRRGNQTALCGGGIQTREVYCVQANENLLSQLSTHKNKEASKPM
DLKLCTGPIPNTTQLCHIPCPTECEVSPWSAWGPCTYENCNDQQGKKGFKLRKRRITNEP
TGGSGVTGNCPHLLEAIPCEEPACYDWKAVRLGDCEPDNGKECGPGTQVQEVVCINSDGE
EVDRQLCRDAIFPIPVACDAPCPKDCVLSTWSTWSSCSHTCSGKTTEGKQIRARSILAYA
GEEGGIRCPNSSALQEVRSCNEHPCTVYHWQTGPWGQCIEDTSVSSFNTTTTWNGEASCS
VGMQTRKVICVRVNVGQVGPKKCPESLRPETVRPCLLPCKKDCIVTPYSDWTSCPSSCKE
GDSSIRKQSRHRVIIQLPANGGRDCTDPLYEEKACEAPQACQSYRWKTHKWRRCQLVPWS
VQQDSPGAQEGCGPGRQARAITCRKQDGGQAGIHECLQYAGPVPALTQACQIPCQDDCQL
TSWSKFSSCNGDCGAVRTRKRTLVGKSKKKEKCKNSHLYPLIETQYCPCDKYNAQPVGNW
SDCILPEGKVEVLLGMKVQGDIKECGQGYRYQAMACYDQNGRLVETSRCNSHGYIEEACI
IPCPSDCKLSEWSNWSRCSKSCGSGVKVRSKWLREKPYNGGRPCPKLDHVNQAQVYEVVP
CHSDCNQYLWVTEPWSICKVTFVNMRENCGEGVQTRKVRCMQNTADGPSEHVEDYLCDPE
EMPLGSRVCKLPCPEDCVISEWGPWTQCVLPCNQSSFRQRSADPIRQPADEGRSCPNAVE
KEPCNLNKNCYHYDYNVTDWSTCQLSEKAVCGNGIKTRMLDCVRSDGKSVDLKYCEALGL
EKNWQMNTSCMVECPVNCQLSDWSPWSECSQTCGLTGKMIRRRTVTQPFQGDGRPCPSLM
DQSKPCPVKPCYRWQYGQWSPCQVQEAQCGEGTRTRNISCVVSDGSADDFSKVVDEEFCA
DIELIIDGNKNMVLEESCSQPCPGDCYLKDWSSWSLCQLTCVNGEDLGFGGIQVRSRPVI
IQELENQHLCPEQMLETKSCYDGQCYEYKWMASAWKGSSRTVWCQRSDGINVTGGCLVMS
QPDADRSCNPPCSQPHSYCSETKTCHCEEGYTEVMSSNSTLEQCTLIPVVVLPTMEDKRG
DVKTSRAVHPTQPSSNPAGRGRTWFLQPFGPDGRLKTWVYGVAAGAFVLLIFIVSMIYLA
CKKPKKPQRRQNNRLKPLTLAYDGDADM (SEQ ID NO: 41)

Figure 16. Nucleotide and Protein Sequences for CG50817-04.

>CG50817-04 1447 nt

GCGGACACCAGTGATGCTCCTGGGACCCTACGCAATCTGCGCCTGCGTCTCATCAGTCGC
CCCACATGTAACTGTATCTACAACCAGCTGCACCAGCGACACCTGTCCAACCCGGCCCGG
CCTGGGATGCTATGTGGGGGCCCCCAGCCTGGGGTGCAGGGCCCCTGTCAGGTCTGATAG
GGAGAAGAGAAGGAGCAGAAGGGGAGGGGCCTAACCCTGGGCTGGGGTTGGACTCACAG
GACTGGGGGAAAGAGCTGCAATCAGAGGGTGTCTGCCATAGCTGGGCTCAGGCATCTGTC
CTTGGCTTTGTTGCCTGGCTCCAGGGAGATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCT
GACGGACACTGGGTTCAGGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGAC
GCTCCTGTGCTGCTGACCAACACAGCTGCTCACAGTTCCTGGCTGCAGGCTCGAGTTCAG
GGGGCAGCTTTCCTGGCCCAGAGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGT
GTAGCCTGTGGATCCTTGAGGACAGCAGGTCCCCAGGCAGGAGCACCCTCCCCATGGCCC
TGGGAGGCCAGGCTGATGCACCAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTCAGAG
GAGGCGGTGCTAACTGCTGCCCACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGC
GTAGGGCTGGGGACCAGACCGGAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCC
TACACCCACCCTGAGGGGGGCTACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACA
CTGGGAGCCAGCCTGCGGCCCCTCTGCCTGCCCTATGCTGACCACCACCTGCCTGATGGG
GAGCGTGGCTGGGTTCTGGGACGGGCCCGCCCAGGAGCAGGCATCAGCTCCCTCCAGACA
GTGCCCGTGACCCTCCTGGGGCCTAGGGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGT
GATGGCAGCCCTATTCTGCCGGGGATGGTGTGTACCAGTGCTGTGGGTGAGCTGCCCAGC
TGTGAGGCCAACCAACCAGCTGCTGACAGGGGACCTGGCCATTCTCAGGAACAAGAGAAT
GCAGGCAGGCAAATGGCATTACTGCCCCTGTCCTCCCCACCCTGTCATGTGTGATTCCAG
GCACCAGGGCAGGCCCAGAAGCCCAGCAGCTGTGGGAAGGAACCTGCCTGGGGCCACAGG
TGCCCACTCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCCCACACCCAACTCTGC
TACCAAGCAGGCGTCTCAGCTTTCCTCCTCCTTTACCCTTTCAGATACAATCACGCCAGC
CACGTTGTTTTGAAAATTTCTTTTTTTGGGGGGCAGCAGTTTTCCTTTTTTTAAACTTAA
ATAAATT (SEQ ID NO:42)

Protein Sequence for CG50817-04 ORF Start: 520 ORF Stop: 1192 Frame: 1

Protein Sequence:

>CG50817-04-prot 224 aa

MSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGR
QAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYA
DHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGMVCTS
AVGELPSCEANQPAADRGPGHSQEQENAGRQMALLPLSSPPCHV (SEQ ID NO:43)

Figure 17. Nucleotide and Protein Sequences for CG50817-05.

. Nucleotide sequence encoding the Peptidase-like protein of the invention.

>CG50817-05
CGCTGGGCCTCTGTCCTG**ATG**CTGCTGAGCTCCCTGGTGTCTCTCGCTGGTTCTGTCTAC 60
CTGGCCTGGATCCTGTTCTTCGTGCTCTATGATTTCTGCATTGTTTGTATCACCACCTAT 120
GCTATCAACGTGAGCCTGATGTGGCTCAGTTTCCGGAAGGTCCAAGAACCCCAGGGCCAA 180
CCCAAGCCTCAGGAGGGCAACACAGTCCCTGGCGAGTGGCCCTGGCAGGCCAGTGTGAGG 240
AGGCAAGGAGCCCACATCTGCAGCGGCTCCCTGGTGGCAGACACCTGGGTCCTCACTGCT 300
GCCCACTGCTTTGAAAAGGCAGCAGCAACAGAACTGAATTCCTGCGTGAGGGACTCAGCC 360
CCTGGGGCCGAAGAGGTGGGGGTGGCTGCCCTGCAGTTGCCCAGGGCCTATAACCACTAC 420
AGCCAGGGCTCAGACCTGGCCCTGCTGCAGCTCGCCCACCCCACGACCCACACACCCCTC 480
TGCCTGCCCCAGCCCGCCCATCGCTTCCCCTTTGGAGCCTCCTGCTGGGCCACTGGCTGG 540
GATCAGGACACCAGTGATGCTCCTGGGACCCTACGCAATCTGCGCCTGCGTCTCATCAGT 600
CGCCCCACATGTAACTGTATCTACAACCAGCTGCACCAGCGACACCTGTCCAACCCGGCC 660
CGGCCTGGGATGCTATGTGGGGGCCCCCAGCCTGGGGTGCAGGGCCCCTGTCAGGGAGAT 720
TCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGACACTGGGTTCAGGCTGGCATCATC 780
AGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTGTGCTGCTGACCAACACAGCTGCT 840
CACAGTTCCTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTTTCCTGGCCCAGAGCCCAGAG 900
ACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGATCCTTGAGGACAGCAGGT 960
CCCCAGGCAGGAGCACCCTCCCCATGGCCCTGGGAGGCCAGGCTGATGCACCAGGGACAG 1020
CTGGCCTGTGGCGGAGCCCTGGTGTCAGAGGAGGCGGTGCTAACTGCTGCCCACTGCTTC 1080
ATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGACCGGAGGAGTGG 1140
GGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGGCTACGACATG 1200
GCCCTCCTGCTGCTGGCCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCCCTCTGCCTG 1260
CCCTATGCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTTCTGGGACGGGCCCGC 1320
CCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCTCCTGGGGCCTAGGGCC 1380
TGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCGGGGATGGTG 1440
TGTACCAGTGCTGTGGGTGAGCTGCCCAGCTGTGAGGCCAACCAACCAGCTGCTGACAGG 1500
GGACCTGGCCATTCTCAGGAACAAGAGAATGCAGGCAGGCAAATGGCATTACTGCCCCTG 1560
TCCTCCCCACCCTGTCATGTGT**GA**TTCCAGGC 1592
(SEQ ID NO:44)

Protein sequence encoded by the coding sequence shown above.

>CG50817-05
MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGQPKPQEG 60
NTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSCVRDSAPGAEEV 120
GVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATGWDQDTSD 180
APGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVL 240
CLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSPETPEMSD 300
EDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGRQAP 360
EEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYADHH 420
LPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGMVCTSAVG 480
ELPSCEANQPAADRGPGHSQEQENAGRQMALLPLSSPPCHV 521
(SEQ ID NO:45)

Figure 18. Nucleotide and Protein Sequences for CG50817-06.

Nucleotide sequence encoding the Peptidase-like protein of the invention.

>CG50817-06
<u>AGCGACACCTGTCCAACCCGGCCCGGCCTGGG</u>**ATG**CTATGTGGGGGCCCCCAGCCTGGGG 60
TGCAGGGCCCCTGTCAGGGAGATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGAC 120
ACTGGGTTCAGGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTG 180
TGCTGCTGACCAACACAGCTGCTCACAGTTCCTGGCTGCAGGCTCGAGTTCAGGGGGCAG 240
CTTTCCTGGCCCAGAGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCT 300
GTGGATCCTTGAGGACAGCAGGTCCCCAGGCAGGAGCACCCTCCCCATGGCCCTGGGAGG 360
CCAGGCTGATGCACCAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTCAGAGGAGGCGG 420
TGCTAACTGCTGCCCACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGC 480
TGGGGACCAGACCGGAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCC 540
ACCCTGAGGGGGGCTACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACACTGGGAG 600
CCAGCCTGCGGCCCCTCTGCCTGCCCTATGCTGACCACCACCTGCCTGATGGGGAGCGTG 660
GCTGGGTTCTGGGACGGGCCCGCCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCG 720
TGACCCTCCTGGGGCCTAGGGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCA 780
GCCCTATTCTGCCGGGGATGGTGTGTACCAGTGCTGTGGGTGAGCTGCCCAGCTGTGAGG 840
CCAACCAACCAGCTGCTGACAGGGGACCTGGCCATTCTCAGGAACAAGAGAATGCAGGCA 900
GGCAAATGGCATTACTGCCCCTGTCCTCCCCACCCTGTCATGTG**TGA**<u>TTCCAGGCACCAG</u> 960
<u>GGCAGGCCCAGAAGCCCAGCAGCTGTGGGAAGGAACCTGCCTGGGGCCACAGGTGCCCAC</u> 1020
<u>TCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCCCACACCCAACTCTGCTACCAAG</u> 1080
<u>CAGGCGTCTCAGCTTTCCTCCTCCTTTACCCTTTCAGATACAATCACGCCAGCCACGTTG</u> 1140
<u>TTTTGAAAATTTCTTTTTTTGGGGGGCAGCAGTTTTCCTTTTTTTAAACTTAAATAAATT</u> 1200
(SEQ ID NO:46)

Protein sequence encoded by the coding sequence shown above.

>CG50817-06
MLCGGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSS 60
WLQARVQGAAFLAQSPETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLAC 120
GGALVSEEAVLTAAHCFIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALL 180
LLAQPVTLGASLRPLCLPYADHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSR 240
LHAAPGGDGSPILPGMVCTSAVGELPSCEANQPAADRGPGHSQEQENAGRQMALLPLSSP 300
PCHV 304
(SEQ ID NO:47)

Figure 19. Nucleotide and Protein Sequences For CG51099-03.

Nucleotide sequence encoding the Serine Protease-like protein of the invention.

```
>CG51099-03
CGGAGAGACGCAGTCGGCTGCCACCCCGGGATGGGTCGCTGGTGCCAGACCGTCGCGCGC      60
GGGCAGCGCCCCCGGACGTCTGCCCCCTCCCGCGCCGGTGCCCTGCTGCTGCTGCTTCTG     120
TTGCTGAGGTCTGCAGGTTGCTGGGGCGCAGGGGAAGCCCCGGGGGCGCTGTCCACTGCT     180
GATCCCGCCGACCAGAGCGTCCAGTGTGTCCCCAAGGCCACCTGTCCTTCCAGCCGGCCT     240
CGCCTTCTCTGGCAGACCCCGACCACCCAGACACTGCCCTCGACCACCATGGAGACCCAA     300
TTCCCAGTTTCTGAAGGCAAAGTCGACCCATACCGCTCCTGTGGCTTTTCCTACGAGCAG     360
GACCCCACCCTCAGGGACCCAGAAGCCGTGGCTCGGCGGTGGCCCTGGATGGTCAGCGTG     420
CGGGCCAATGGCACACACATCTGTGCCGGCACCATCATTGCCTCCCAGTGGGTGCTGACT     480
GTGGCCCACTGCCTGATCTGGCGTGATGTTATCTACTCAGTGAGGGTGGGGAGTCCGTGG     540
ATTGACCAGATGACGCAGACCGCCTCCGATGTCCCGGTGCTCCAGGTCATCATGCATAGC     600
AGGTACCGGGCCCAGCGGTTCTGGTCCTGGGTGGGCCAGGCCAACGACATCGGCCTCCTC     660
AAGCTCAAGCAGGAACTCAAGTACAGCAATTACGTGCGGCCCATCTGCCTGCCTGGCACG     720
GACTATGTGTTGAAGGACCATTCCCGCTGCACTGTGACGGGCTGGGGACTTTCCAAGGCT     780
GACGGCATGTGGCCTCAGTTCCGGACCATTCAGGAGAAGGAAGTCATCATCCTGAACAAC     840
AAAGAGTGTGACAATTTCTACCACAACTTCACCAAAATCCCCACTCTGGTTCAGATCATC     900
AAGTCCCAGATGATGTGTGCGGAGGACACCCACAGGGAGAAGTTCTGCTATGAGCTAACT     960
GGAGAGCCCTTGGTCTGCTCCATGGAGGGCACGTGGTACCTGGTGGGATTGGTGAGCTGG    1020
GGTGCAGGCTGCCAGAAGAGCGAGGCCCCACCCATCTACCTACAGGTCTCCTCCTACCAA    1080
CACTGGATCTGGGACTGCCTCAACGGGCAGGCCCTGGCCCTGCCAGCCCCATCCAGGACC    1140
CTGCTCCTGGCACTCCCACTGCCCCTCAGCCTCCTTGCTGCCCTCTGACTCTGTGTGCCC    1200
TCCCTCACTTGTGA                                                  1214
(SEQ ID NO:48)
```

Protein sequence encoded by the nucleotide sequence shown above.

```
>CG51099-03
MGRWCQTVARGQRPRTSAPSRAGALLLLLLLLRSAGCWGAGEAPGALSTADPADQSVQCV  60
PKATCPSSRPRLLWQTPTTQTLPSTTMETQFPVSEGKVDPYRSCGFSYEQDPTLRDPEAV  120
ARRWPWMVSVRANGTHICAGTIIASQWVLTVAHCLIWRDVIYSVRVGSPWIDQMTQTASD  180
VPVLQVIMHSRYRAQRFWSWVGQANDIGLLKLKQELKYSNYVRPICLPGTDYVLKDHSRC  240
TVTGWGLSKADGMWPQFRTIQEKEVIILNNKECDNFYHNFTKIPTLVQIIKSQMMCAEDT  300
HREKFCYELTGEPLVCSMEGTWYLVGLVSWGAGCQKSEAPPIYLQVSSYQHWIWDCLNGQ  360
ALALPAPSRTLLLALPLPLSLLAAL                                     385 (SEQ ID NO:49)
```

Figure 20. Nucleotide and Protein Sequences For CG57051-04.

Nucleotide sequence encoding the Angiopoietin-like protein, CG57051-04.

>CG57051-04
TGCGGATCCTCACACGACTGTGATCCGATTCTTTCCAGCGGCTTCTGCAACCAAGCGGGT 60
CTTACCCCCGGTCCTCCGCGTCTCCAGTCCTCGCACCTGGAACCCCAACGTCCCCGAGAG 120
TCCCCGAATCCCCGCTCCCAGGCTACCTAAGAGG**ATG**AGCGGTGCTCCGACGGCCGGGGC 180
AGCCCTGATGCTCTGCGCCGCCACCGCCGTGCTACTGAGCGCTAGATCTGGACCCGTGCA 240
GTCCAAGTCGCCGCGCTTTGCGTCCTGGGACGAGATGAATGTCCTGGCGCACGGACTCCT 300
GCAGCTCGGCCAGGGGCTGCGCGAACACGCGGAGCGCACCCGCAGTCAGCTGAGCGCGCT 360
GGAGCGGCGCCTGAGCGCGTGCGGGTCCGCCTGTCAGGGAACCGAGGGGTCCACCGACCT 420
CCCGTTAGCCCCTGAGAGCCGGGTGGACCCTGAGGTCCTTCACAGCCTGCAGACACAACT 480
CAAGGCTCAGAACAGCAGGATCCAGCAACTCTTCCACAAGGTGGCCCAGCAGCAGCGGCA 540
CCTGGAGAAGCAGCACCTGCGAATTCAGCATCTGCAAAGCCAGTTTGGCCTCCTGGACCA 600
CAAGCACCTAGACCATGAGGTGGCCAAGCCTGCCCGAAGAAAGAGGCTGCCCGAGATGGC 660
CCAGCCAGTTGACCCGGCTCACAATGTCAGCCGCCTGCACCGAGGCTGGTGGTTTGGCAC 720
CTGCAGCCATTCCAACCTCAACGGCCAGTACTTCCGCTCCATCCCACAGCAGCGGCAGAA 780
GCTTAAGAAGGGAATCTTCTGGAAGACCTGGCGGGGCCGCTACTACCCGCTGCAGGCCAC 840
CACCATGTTGATCCAGCCCATGGCAGCAGAGGCAGCCTCC**TAG**CGTCCTGGCTGGGCCTG 900
GTCCCAGGCCCACGAAAGACGGTGACTCTTGGCTCTG 937 (SEQ ID NO:50)

Protein sequence encoded by the nucleotide sequence shown above.

>CG57051-04
MSGAPTAGAALMLCAATAVLLSARSGPVQSKSPRFASWDEMNVLAHGLLQLGQGLREHAE 60
RTRSQLSALERRLSACGSACQGTEGSTDLPLAPESRVDPEVLHSLQTQLKAQNSRIQQLF 120
HKVAQQQRHLEKQHLRIQHLQSQFGLLDHKHLDHEVAKPARRKRLPEMAQPVDPAHNVSR 180
LHRGWWFGTCSHSNLNGQYFRSIPQQRQKLKKGIFWKTWRGRYYPLQATTMLIQPMAAEA 240
AS 242 (SEQ ID NO:51)

Figure 21. Nucleotide and Protein Sequences For CG57051-05.

Nucleotide sequence encoding the Angiopoietin-like protein, CG57051-05.

>CG57051-05
CTTCGTCTCCAGTCCTCGCACCTGGAACCCCAACGTCCCCGAGAGTCCCCGAATCCCCGC 60
TCCCAGGCTACCTAAGAGG**ATG**AGCGGCGCTCCGACGGCCGGGGCAGCCCTGATGCTCTG 120
CGCCGCCACCGCCGTGCTACTGAGCGCTCAGGGCGGACCCGTGCAGTCCAAGTCGCCGCG 180
CTTTGCGTCCTGGGACGAGATGAATGTCCTGGCGCACGGACTCCTGCAGCTCGGCCAGGG 240
GCTGCGCGAACACGCGGAGCGCACCCGCAGTCAGCTGAGCGCGCTGGAGCGGCGCCTGAG 300
CGCGTGCGGGTCCGCCTGTCAGGGAACCGAGGGGTCCACCGACCTCCCGTTAGCCCCTGA 360
GAGCCGGGTGGACCCTGAGGTCCTTCACAGCCTGCAGACACAACTCAAGGCTCAGAACAG 420
CAGGATCCAGCAACTCTTCCACAAGGTGGCCCAGCAGCAGCGGCACCTGGAGAAGCAGCA 480
CCTGCGAATTCAGCATCTGCAAAGCCAGTTTGGCCTCCTGGACCACAAGCACCTAGACCA 540
TGAGGGTGGCAAGCCTGCCCGAAGAAAGAGGCTGCCCGAGATGGCCCAGCCAGTTGACCC 600
GGCTCACAATGTCAGCCGCCTGCACCATGGAGGCTGGACAGTAATTCAGAGGCGCCACGA 660
TGGCTCAGTGGACTTCAACCGGCCCTGGGAAGCCTACAAGGCGGGGTTTGGGGATCCCCA 720
CGGCGAGTTCTGGCTGGGTCTGGAGAAGGTGCATAGCATCATGGGGGACCGCAACAGCCG 780
CCTGGCCGTGCAGCTGCGGGACTGGGATGGCAACGCCGAGTTGCTGCAGTTCTCCGTGCA 840
CCTGGGTGGCGAGGACACGGCCTATAGCCTGCAGCTCACTGCACCCGTGGCCGGCCAGCT 900
GGGCGCCACCACCGTCCCACCCAGCGGCCTCTCCGTACCCTTCTCCACTTGGGACCAGGA 960
TCACGACCTCCGCAGGGACAAGAACTGCGCCAAGAGCCTCTCTGGAGGCTGGTGGTTTGG 1020
CACCTGCAGCCATTCCAACCTCAACGGCCAGTACTTCCGCTCCATCCCACAGCAGCGGCA 1080
GAAGCTTAAGAAGGGAATCTTCTGGAAGACCTGGCGGGGCCGCTACTACCCGCTGCAGGC 1140
CACCACCATGTTGATCCAGCCCATGGCAGCAGAGGCAGCCTCC**TAG**CGTCCTGGCTGGGC 1200
CTGGTCCCAGGCCCACGAAAGAGGTGACTCTTGGCTCTG 1239 (SEQ ID NO:52)

Protein sequence for Angiopoietin-like protein, CG57051-05.

>CG57051-05
MSGAPTAGAALMLCAATAVLLSAQGGPVQSKSPRFASWDEMNVLAHGLLQLGQGLREHAE 60
RTRSQLSALERRLSACGSACQGTEGSTDLPLAPESRVDPEVLHSLQTQLKAQNSRIQQLF 120
HKVAQQQRHLEKQHLRIQHLQSQFGLLDHKHLDHEGGKPARRKRLPEMAQPVDPAHNVSR 180
LHHGGWTVIQRRHDGSVDFNRPWEAYKAGFGDPHGEFWLGLEKVHSIMGDRNSRLAVQLR 240
DWDGNAELLQFSVHLGGEDTAYSLQLTAPVAGQLGATTVPPSGLSVPFSTWDQDHDLRRD 300
KNCAKSLSGGWWFGTCSHSNLNGQYFRSIPQQRQKLKKGIFWKTWRGRYYPLQATTMLIQ 360
PMAAEAAS 368 (SEQ ID NO:53)

Figure 22. Nucleotide and Protein Sequences For CG57051-02.

Nucleotide sequence encoding the Angiopoietin-like protein of the invention.

```
>CG57051_02
TGCGGATCCTCACACGACTGTGATCCGATTCTTTCCAGCGGCTTCTGCAACCAAGCGGGT     60
CTTACCCCCGGTCCTCCGCGTCTCCAGTCCTCGCACCTGGAACCCCAACGTCCCCGAGAG    120
TCCCCGAATCCCCGCTCCCAGGCTACCTAAGAGGATGAGCGGTGCTCCGACGGCCGGGGC    180
AGCCCTGATGCTCTGCGCCGCCACCGCCGTGCTACTGAGCGCTAGATCTGGACCCGTGCA    240
GTCCAAGTCGCCGCGCTTTGCGTCCTGGGACGAGATGAATGTCCTGGCGCACGGACTCCT    300
GCAGCTCGGCCAGGGGCTGCGCGAACACGCGGAGCGCACCCGCAGTCAGCTGAGCGCGCT    360
GGAGCGGCGCCTGAGCGCGTGCGGGTCCGCCTGTCAGGGAACCGAGGGGTCCACCGACCT    420
CCCGTTAGCCCCTGAGAGCCGGGTGGACCCTGAGGTCCTTCACAGCCTGCAGACACAACT    480
CAAGGCTCAGAACAGCAGGATCCAGCAACTCTTCCACAAGGTGGCCCAGCAGCAGCGGCA    540
CCTGGAGAAGCAGCACCTGCGAATTCAGCATCTGCAAAGCCAGTTTGGCCTCCTGGACCA    600
CAAGCACCTAGACCATGAGGTGGCCAAACCTGCCCGAAGAAAGAGGCTGCCCGAGATGGC    660
CCAGCCAGTTGACCCGGCTCACAATGTCAGCCGCCTGCACCATGGAGGCTGGACAGTAAT    720
TCAGAGGCGCCACGATGGCTCAATGGACTTCAACCGGCCCTGGGAAGCCTACAAGGCGGG    780
GTTTGGGGATCCCCACGGCGAGTTCTGGCTGGGTCTGGAGAAGGTGCATAGCATCACGGG    840
GGACCGCAACAGCCGCCTGGCCGTGCAGCTGCGGGACTGGGATGGCAACGCCGAGTTGCT    900
GCAGTTCTCCGTGCACCTGGGTGGCGAGGACACGGCCTATAGCCTGCAGCTCACTGCACC    960
CGTGGCCGGCCAGCTGGGCGCCACCACCGTCCCACCCAGCGGCCTCTCCGTACCCTTCTC   1020
CACTTGGGACCAGGATCACGACCTCCGCAGGGACAAGAACTGCGCCAAGAGCCTCTCTGC   1080
CCCATCGGTGGCTCAAAGACCTGACCATGTTCCCTCTCCCCTGACCCCGGCAGGAGGCTG   1140
GTGGTTTGGCACCTGCAGCCATTCCAACCTCAACGGCCAGTACTTCCGCTCCATCCCACA   1200
GCAGCGGCAGAAGCTTAAGAAGGGAATCTTCTGGAAGACCTGGCGGGGCCGCTACTACCC   1260
GCTGCAGGCCACCACCATGTTGATCCAGCCCATGGCAGCAGAGGCAGCCTCCTAG   1315
(SEQ ID NO:54)
```

Protein sequence for CG57051-02.

```
>CG57051_02
MSGAPTAGAALMLCAATAVLLSARSGPVQSKSPRFASWDEMNVLAHGLLQLGQGLREHAE     60
RTRSQLSALERRLSACGSACQGTEGSTDLPLAPESRVDPEVLHSLQTQLKAQNSRIQQLF    120
HKVAQQQRHLEKQHLRIQHLQSQFGLLDHKHLDHEVAKPARRKRLPEMAQPVDPAHNVSR    180
LHHGGWTVIQRRHDGSMDFNRPWEAYKAGFGDPHGEFWLGLEKVHSITGDRNSRLAVQLR    240
DWDGNAELLQFSVHLGGEDTAYSLQLTAPVAGQLGATTVPPSGLSVPFSTWDQDHDLRRD    300
KNCAKSLSAPSVAQRPDHVPSPLTPAGGWWFGTCSHSNLNGQYFRSIPQQRQKLKKGIFW    360
KTWRGRYYPLQATTMLIQPMAAEAAS    386   (SEQ ID NO:55)
```

Figure 23. Nucleotide and Protein Sequences For CG57051-03.

Nucleotide sequence encoding the Angiopoietin-like protein, CG57051-03.

```
>CG57051-03
CCCCGAGAGTCCCCGAATCCCCGCTCCCAGGCTACCTAAGAGGATGAGCGGTGCTCCGAC    60
GGCCGGGGCAGCCCTGATGCTCTGCGCCGCCACCGCCGTGCTACTGAGCGCTCAGGGCGG   120
ACCCGTGCAGTCCAAGTCGCCGCGCTTTGCGTCCTGGGACGAGATGAATGTCCTGGCGCA   180
CGGACTCCTGCAGCTCGGCCAGGGGCTGCGCGAACACGCGGAGCGCACCCGCAGTCAGCT   240
GAGCGCGCTGGAGCGGCGCCTGAGCGCGTGCGGGTCCGCCTGTCAGGGAACCGAGGGGTC   300
CACCGACCTCCCGTTAGCCCCTGAGAGCCGGGTGGACCCTGAGGTCCTTCACAGCCTGCA   360
GACACAACTCAAGGCTCAGAACAGCAGGATCCAGCAACTCTTCCACAAGGTGGCCCAGCA   420
GCAGCGGCACCTGGAGAAGCAGCACCTGCGAATTCAGCATCTGCAAAGCCAGTTTGGCCT   480
CCTGGACCACAAGCACCTAGACCATGAGGTGGCCAAGCCTGCCCGAAGAAAGAGGCTGCC   540
CGAGATGGCCCAGCCAGTTGACCCGGCTCACAATGTCAGCCGCCTGCACCATGGAGGCTG   600
GACAGTAATTCAGAGGCGCCACGATGGCTCAGTGGACTTCAACCGGCCCTGGGAAGCCTA   660
CAAGGCGGGGTTTGGGGATCCCCACGGCGAGTTCTGGCTGGGTCTGGAGAAGGTCCATAG   720
CATCACGGGGGACCGCAACAGCCGCCTGGCCGTGCAGCTGCGGGACTGGGATGACAACGC   780
CGAGTTGCTGCAGTTCTCCGTGCACCTGGGTGGCGAGGACACGGCCTATAGCCTGCAGCT   840
CACTGCACCCGTGGCCGGCCAGCTGGGCGCCACCACCGTCCCACCCAGCGGCCTCTCCGT   900
ACCCTTCCCCACTTGGGACCAGGATCACGACCTCCGCAGGGACAAGAACTGCGCCAAGAG   960
CCTCTCTGGAGGCTGGTGGTTTGGCACCTGCAGCCATTCCAACCTCAACGGCCAGTACTT  1020
CCGCTCCATCCCACAGCAGCGGCAGAAGCTTAAGAAGGGAATCTTCTGGAAGACCTGGCG  1080
GGGCCGCTACTACCCGCTGCAGGCCACCACCATGTTGATCCAGCCCATGGCAGCAGAGGC  1140
AGCCTCCTAG   1150 (SEQ ID NO:56)
```

Protein sequence for CG57051-03.

```
>CG57051-03
MSGAPTAGAALMLCAATAVLLSAQGGPVQSKSPRFASWDEMNVLAHGLLQLGQGLREHAE    60
RTRSQLSALERRLSACGSACQGTEGSTDLPLAPESRVDPEVLHSLQTQLKAQNSRIQQLF   120
HKVAQQQRHLEKQHLRIQHLQSQFGLLDHKHLDHEVAKPARRKRLPEMAQPVDPAHNVSR   180
LHHGGWTVIQRRHDGSVDFNRPWEAYKAGFGDPHGEFWLGLEKVHSITGDRNSRLAVQLR   240
DWDDNAELLQFSVHLGGEDTAYSLQLTAPVAGQLGATTVPPSGLSVPFPTWDQDHDLRRD   300
KNCAKSLSGGWWFGTCSHSNLNGQYFRSIPQQRQKLKKGIFWKTWRGRYYPLQATTMLIQ   360
PMAAEAAS   368 (SEQ ID NO:57)
```